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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:20:41 ; Search time 11 Seconds
(without alignments)
227.215 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72

Perfect score: 231
Sequence: 1 RKAMKGLGDEBSILTLTIS.....ISAAPKTLFGRLDLIDKSE 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	231	100.0	319 1 ANX5 HUMAN	P08758 homo sapien
2	224	97.0	320 1 ANX5 BOVIN	P81287 bos taurus
3	207	89.6	319 1 ANX5 MOUSE	P48036 mus musculu
4	206	89.2	321 1 ANX5 CHICK	P17153 gallus galli
5	194	84.0	318 1 ANX5 RAT	P14668 rattus norv
6	179	77.5	323 1 ANX5 CYNPY	P70075 cynops pyr
7	173	74.9	318 1 ANX4 BOVIN	P13714 bos taurus
8	172	74.5	318 1 ANX4 PIG	P08132 sus scrofa
9	170	73.6	618 1 ANX6 BOVIN	P79134 bos taurus
10	169	73.2	463 1 ANX7 MOUSE	P07076 mus musculu
11	167	72.3	318 1 ANX4 HUMAN	P09525 homo sapien
12	167	72.3	672 1 ANX6 HUMAN	P08133 homo sapien
13	166	71.9	671 1 ANX6 CHICK	P51901 gallus galli
14	165	71.4	318 1 ANX4 CANFA	P50594 canis fami1
15	164	71.0	672 1 ANX6 MOUSE	P14824 mus musculu
16	163	70.6	318 1 ANX4 RAT	P55260 rattus norv
17	163	70.6	466 1 ANX7 HUMAN	P20073 homo sapien
18	162	70.1	318 1 ANX4 MOUSE	P97429 mus musculu
19	162	70.1	672 1 ANX6 RAT	P48037 rattus norv
20	159	68.8	503 1 ANXB BOVIN	P27214 bos taurus
21	159	68.8	503 1 ANXB MOUSE	P97384 mus musculu
22	159	68.8	503 1 ANXB RABIT	P31477 coryctolagus
23	159	68.8	505 1 ANXB HUMAN	P50995 homo sapien
24	156	67.5	316 1 ANXC HYDAT	P26256 hydat atten
25	150	64.9	327 1 ANX8 HUMAN	P13928 homo sapien
26	150	64.9	327 1 ANX8 MOUSE	O92125 xenopus lae
27	149.5	64.7	512 1 ANX7 XENLA	O92125 xenopus lae
28	148	64.1	324 1 ANX9 DROME	P22464 drosophila
29	141	61.0	320 1 ANXX DROME	P22465 drosophila
30	131	56.7	323 1 ANX3 HUMAN	P12429 homo sapien
31	129	55.8	323 1 ANX3 MOUSE	O35639 mus musculu
32	124	53.7	324 1 ANX3 RAT	P14669 rattus norv
33	120	51.9	462 1 ANX7 DICDI	P24639 dictyostell

34	119	51.5	345 1 ANX1 RAT
35	118	51.1	345 1 ANX1 MOUSE
36	116	50.2	345 1 ANX1 HORSE
37	115	49.8	314 1 ANX4 PRAN
38	115	49.8	315 1 ANX0 CANFA
39	112	48.5	338 1 ANX2 BOVIN
40	112	48.5	343 1 ANI2 COLLI
41	111	48.1	338 1 ANX2 HUMAN
42	111	48.1	338 1 ANX2 MOUSE
43	111	48.1	338 1 ANX2 RAT
44	111	48.1	346 1 ANX1 RABIT
45	110	47.6	324 1 ANXA HUMAN

ALIGNMENTS

RESULT 1	ID	ANX5 HUMAN	STANDARD;	PRT;	319 AA.
AC	P08758;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-NOV-1988 (Rel. 09, Last annotation update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (CBP-1) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplasticin inhibitor) (Vascular anticoagulant- α) (VAC- α (Anchoring CII))				
DE	ANKX5 OR ANX5 OR ENX2 OR PP4.				
GN	Homo sapiens (Human).				
OS	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=88234495; Pubmed=2967495;				
RA	Grundmann U., Abel K.-D., Bohn H., Loebermann H., Lottspeich F., Kuempfer H.;				
RT	"Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).				
LN	[2]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RP	MEDLINE=88271329; Pubmed=2455636;				
RA	Wauter-Fogt I., Reutelingersperger C.P.M., Pieters J., Bodo G., Strietowa C., Hauptmann R.;				
RT	"Cloning and expression of cDNA for human vascular Ca ²⁺ -dependent phospholipid-binding protein.";				
RL	Eur. J. Biochem. 174:585-592(1988).				
LN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=88273202; Pubmed=2968983;				
RA	Repinaky R.B., Tizard R., Mattalino R.J., Sinclair L.K., Miller G.T., Brownin J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter I., Hession C., Frey A.Z., Wallner B.P.;				
RT	"Five distinct calcium and phospholipid binding proteins share homology with lipocortin I.";				
RL	J. Biol. Chem. 263:10799-10811(1988).				
LN	[4]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=88163463; Pubmed=2964863;				
RA	Funkosohi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;				
RT	"Primary structure of human placental anticoagulant protein.";				
RL	Biochemistry 26:8087-8092(1987).				
LN	[5]				
RP	SEQUENCE FROM N.A., AND SEQUENCE.				
RP	MEDLINE=88139278; Pubmed=2963810;				
RA	Iwasaki A., Suda M., Nakao H., Nagoya T., Saito Y., Arai K., Matsuuchi T., Sato F., Yoshizaki H., Hirata M., Miyata T., Shidara Y., Murata M., Maki M.;				
RT	"Structure and expression of cDNA for an inhibitor of blood coagulation isolated from human placenta: a new lipocortin-like protein.";				
RL					

P07150	rattus r
P10107	mus musc
O8hzm6	equus ca
P51074	fragaria
O29471	canis fa
B04272	bos tau
O92040	columba
P07355	homo sap
P07356	mus mus
O07936	rattus
P51652	oryctol
G9u712	homo sa

RL J. Biochem. 102:1261-1273(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228020; PubMed=2967291;
RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
RT "Cloning and expression of cDNA for human endonexin II, a Ca²⁺ and
RT phospholipid binding protein.";
RL J. Biol. Chem. 263:8037-8043(1988).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95047484; PubMed=7958998;
RA Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
RT "The gene encoding human annexin V has a TATA-less promoter with a
RT high G+C content.";
RL Gene 149:253-260(1994).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94307733; PubMed=8034319;
RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
RA Tait J.P.;
RT "Organization of the human annexin V (ANX5) gene.";
RL Genomics 20:463-467(1994).
RN [9]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, Ovary, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchler L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Bailey U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=90088443; PubMed=2532007;
RA Rothhut R., Comera C., Cortial S., Haumont P.-Y., Diep Ie K.H.,
RA Cavadore J.-C., Conard J., Russo-Marie F., Lederer F.;
RT "A 32 kDa lipocortin from human mononuclear cells appears to be
RT identical with the placental inhibitor of blood coagulation.";
RL Biochem. J. 263:929-935(1989).
RN [11]
RP SEQUENCE OF 85-130; 258-296 AND 299-319.
RX MEDLINE=87317598; PubMed=2957692;
RA Schlaepfer D.D., Mehlman T., Burgess W.H., Haigler H.T.;
RT "Structural and functional characterization of endonexin II, a
RT calcium- and phospholipid-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
RN [12]
RP SEQUENCE OF 84-92.
RX MEDLINE=8906652; PubMed=2974032;
RA Ann N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
RA de Haen C.;
RT "sedimentation equilibrium analysis of five lipocortin-related
RT phospholipase A2 inhibitors from human placenta. Evidence against a
RT mechanistically relevant association between enzyme and inhibitor.";
RL J. Biol. Chem. 263:18657-18663(1988).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RX MEDLINE=91065314; PubMed=2147412;
RA Huber R., Roemisch J., Paques E.-P.;
RT "The crystal and molecular structure of human annexin V, an
RT anticoagulant protein that binds to calcium and membranes.";
RL EMBO J. 9:3867-3874(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91085549; PubMed=2148156;
RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
RT "The calcium binding sites in human annexin V by crystal structure
RT analysis at 2.0-A resolution. Implications for membrane binding and
RT calcium channel activity.";
RL FEBS Lett. 275:15-21(1990).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92177413; PubMed=1311770;
RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
RA Luecke H., Roemisch J., Paques E.-P.;
RT "Crystal and molecular structure of human annexin V after refinement.
RT Implications for structure, membrane binding and ion channel
RT formation of the annexin family of proteins.";
RL J. Mol. Biol. 223:683-704(1992).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=98062349; PubMed=9398511;
RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
RT "Crystal structure of annexin V with its ligand K-201 as a calcium
RT channel activity inhibitor.";
RL J. Mol. Biol. 274:16-20(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=98118533; PubMed=9435213;
RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
RT "Residue-specific bioincorporation of non-natural, biologically
RT active amino acids into proteins as possible drug carriers: structure
RT and stability of the per-thioproline mutant of annexin V.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
RN [18]
RP FUNCTION: This protein is an anticoagulant protein that acts as an
RP indirect inhibitor of the thromboplastin-specific complex, which
RP is involved in the blood coagulation cascade.
RP -1- DOMAIN: A pair of annexin repeats may form one binding site for
RP calcium and phospholipid.
RP -1- SIMILARITY: Belongs to the annexin family.
RP -1- SIMILARITY: Contains 4 annexin repeats.
RP -1- CAUTION: This protein has been independently sequenced by at least
RP seven groups under different names!
RP -1- DATABASE: NMR-RD Systems' cytokine source book: Annexin 5;
RP WWW="http://www.rndsystems.com/asp/9_sitebuilder.asp?bodyid=185".
RN [19]
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RP or send an email to license@sb-sib.ch).
RN [20]
RP EMBL: X13454; CAA30985.1; -
RP EMBL: M13384; AAB55545.1; -
RP EMBL: M13366; AAA3570.1; -
RP EMBL: M21731; AAA3166.1; -
RP EMBL: D00172; BAA00122.1; -
RP EMBL: J03745; AAA52386.1; -
RP EMBL: U01691; AAB40047.1; -
RP EMBL: U01681; AAB40047.1; JOINED.
RP EMBL: U01682; AAB40047.1; JOINED.
RP EMBL: U01683; AAB40047.1; JOINED.
RP EMBL: U01685; AAB40047.1; JOINED.
RP EMBL: U01686; AAB40047.1; JOINED.
RP EMBL: U01687; AAB40047.1; JOINED.
RP EMBL: U01689; AAB40047.1; JOINED.
RP EMBL: U01690; AAB40047.1; JOINED.

Query Match 100.0%; Score 231; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 9.2e-21;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1. RKAMKGLTDEESITLTLTSSNRORISAFKTLRGRLDLDKSE 48
DB 24 RKAMKGLTDEESITLTLTSSNRORISAFKTLRGRLDLDKSE 71

RESULT 2

ANX5 BOVIN STANDARD; PRT; 320 AA.
ID ANX5 BOVIN STANDARD; PRT; 320 AA.
AC P81287; 1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchotin CII).
DE ANXAS OR ANX5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RN [1]
RP SEQUENCE.
RC TISSUE=Brain; MEDLINE=93041974; PubMed=1420335;
RX Learmonth M.P., Howell S.A., Harris A.C.M., Ames B., Patel Y., Giambanco I., Bianchi R., Pulla G., Ceccarelli P., Donato R., Green B.N., Altken A.;
RA "Novel isoforms of Cabp 33/37 (annexin V) from mammalian brain: structural and phosphorylation differences that suggest distinct biological roles."
RT Biochim. Biophys. Acta 1160:76-83 (1992).
RU -1- FUNCTION: This protein is an anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood coagulation cascade.
CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
DR HSSP; P08758; 1ANW.
DR PIR; S27214; S27214.
DR InterPro: IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation; Acetylation.
FT INIT MET 0
FT REPEAT 23 83 ANNEXIN 1.
FT REPEAT 95 155 ANNEXIN 2.
FT REPEAT 179 239 ANNEXIN 3.
FT REPEAT 254 314 ANNEXIN 4.
FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).
FT VARIANT 36 36 S -> T.
FT VARIANT 125 125 K -> E.
SQ SEQUENCE 320 AA; 35942 MW; 50FCF18E95F19CB0 CRC64;

Query Match 97.0%; Score 224; DB 1; Length 320;
Best Local Similarity 95.8%; Pred. No. 6.5e-20;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1. RKAMKGLTDEESITLTLTSSNRORISAFKTLRGRLDLDKSE 48
DB 24 RKAMKGLTDEESITLTLTSSNRORISAFKTLRGRLDLDKSE 71

RESULT 3

ANX5 MOUSE STANDARD; PRT; 319 AA.
ID ANX5 MOUSE STANDARD; PRT; 319 AA.
AC P48036; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchotin CII).
DE ANXAS OR ANX5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneal cavity; MEDLINE=96422179; PubMed=8824796;
RX Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
RA Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.P.;
RA Fernandez M.P.;
RT "Mouse annexin V genomic organization includes an endogenous retrovirus."
RU J. Biochem. 337:125-131 (1999).
RU -1- FUNCTION: This protein is an anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood coagulation cascade.
CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -1- SIMILARITY: Contains 4 annexin repeats.
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CC -----
DR EMBL; U29396; AAC52530.1; -
DR EMBL; D63423; BAA09728.1; -
DR EMBL; AJ230108; CAI13092.1; -
DR EMBL; AJ230110; CAI13092.1; JOINED.
DR EMBL; AJ230111; CAI13092.1; JOINED.
DR EMBL; AJ230114; CAI13092.1; JOINED.
DR EMBL; AJ230116; CAI13092.1; JOINED.
DR EMBL; AJ230118; CAI13092.1; JOINED.
DR EMBL; AJ230119; CAI13092.1; JOINED.
DR EMBL; AJ230120; CAI13092.1; JOINED.
DR EMBL; AJ230121; CAI13092.1; JOINED.
DR EMBL; AJ230122; CAI13092.1; JOINED.
DR EMBL; AJ230123; CAI13092.1; JOINED.
DR EMBL; AJ230124; CAI13092.1; JOINED.
DR HSSP; P14668; 1A8B.
DR SWISS-2DPAGE; P48036; MOUSE.
DR MCD; MG1; 106008; Anxas5.

DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Placenta.
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 SQ SEQUENCE 319 AA; 35752 MW; 55055BAF2E1C367 CRC64;
 Query Match 89.6%; Score 207; DB 1; Length 319;
 Best Local Similarity 87.5%; Pred. No. 7.6e-18;
 Matches 42; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RRAMKGLGTEDESILTLRSNAQOEISAAFKTLFGDLDDLKSE 48
 DB 23 RRAMKGLGTEDESLTLRLTSNAQOEIAQEFKTLFGDLVDLKSE 70
 RESULT 4
 ID ANX5 CHICK STANDARD; PRT; 321 AA.
 AC P17153;
 DT 01-AUG-1990 (Rel. 15; Created)
 DT 01-FEB-1996 (Rel. 33; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosaustra; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88186917; PubMed=2833522;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
 Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of anchoring CII, a collagen binding protein isolated
 from chondrocyte membrane.";
 RL J. Biol. Chem. 263:5921-5925 (1988).
 RN [2]
 RP SUGGEST SEQUENCING ERROR.
 RX MEDLINE=90020458; PubMed=2552626;
 RA Moss S.E., Crumpton M.J.;
 RT "Alternative splicing or cloning artefact?";
 RL Trends Biochem. Sci. 14:325-325 (1989).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=90243721; PubMed=2159478;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
 Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of anchoring CII, a collagen binding protein isolated
 from chondrocyte membrane.";
 RL J. Biol. Chem. 265:8344-8344 (1990).
 RN [4]
 RP REVISIONS.
 RA Pfaeffle M., Ruggiero F., Hofmann H., Fernandez M.P., Selmin O.,
 Yamada Y., Garone R., von der Mark K.;
 RL EMBO J. 9:1336-1336 (1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Liver;
 RX MEDLINE=94215900; PubMed=8163186;
 RA Fernandez M.P., Fernandez M.R., Morgan R.O.;
 RT "Structure of the gene encoding anchoring CII (chick annexin V).";

RL Gene 141:179-186 (1994).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=93249384; PubMed=8484740;
 RA Boustead C.M., Brown R., Walker J.H.;
 RT "Isolation, characterization and localization of annexin V from
 chicken liver.";
 RL Biochem. J. 291:601-608 (1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93229489; PubMed=8471604;
 RA Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.;
 RT "Structure of chicken annexin V at 2.25-A resolution.";
 RL Biochemistry 32:3923-3929 (1993).
 CC -!- FUNCTION: Collagen-binding protein.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- SIMILARITY: Belongs to the annexin family.
 CC -!- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL: M30971; AAA48591.1; ALT_SEQ.
 DR EMBL: U01680; AAB39917.1; -.
 DR EMBL: U01671; AAB39917.1; JOINED.
 DR EMBL: U01672; AAB39917.1; JOINED.
 DR EMBL: U01673; AAB39917.1; JOINED.
 DR EMBL: U01675; AAB39917.1; JOINED.
 DR EMBL: U01676; AAB39917.1; JOINED.
 DR EMBL: U01677; AAB39917.1; JOINED.
 DR EMBL: U01678; AAB39917.1; JOINED.
 DR EMBL: U01679; AAB39917.1; JOINED.
 DR PIR: A35381; LUC85.
 DR PDB: 1ALA; 31-OCT-93.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 FT REPEAT 24 84 ANNEXIN 1.
 FT REPEAT 96 156 ANNEXIN 2.
 FT REPEAT 180 240 ANNEXIN 3.
 FT REPEAT 255 315 ANNEXIN 4.
 FT CONFLICT 168 168 D -> E (IN REF. 1).
 FT TURN 13 14
 FT TURN 17 28
 FT HELIX 35 44
 FT HELIX 47 61
 FT HELIX 65 72
 FT HELIX 75 85
 FT TURN 88 90
 FT HELIX 91 100
 FT HELIX 107 116
 FT HELIX 119 133
 FT HELIX 137 144
 FT HELIX 147 157
 FT TURN 158 158
 FT HELIX 169 184
 FT TURN 185 187
 FT HELIX 191 200
 FT HELIX 203 217
 FT HELIX 221 224
 FT HELIX 232 245
 FT HELIX 247 259

FT HELIX 266 275
 FT TURN 276 280
 FT HELIX 281 292
 FT HELIX 296 303
 FT HELIX 306 316
 SQ SEQUENCE 321 AA; 36198 MW; 43E2983F86797025 CRC64;
 Query Match 89.2%; Score 206; DB 1; Length 321;
 Best Local Similarity 83.3%; Pred. No. 1e-17;
 Matches 40; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKAMKGLTDEESITLTITSRNMQREISAFAFTLFDRLDDIKSE 48
 25 RKAMKGLTDEESITLTITSRNMQREISAFAFTLFDRLDDIKSE 72

RESULT 5

ANX5 RAT STANDARD; PRT: 318 AA.
 ID ANX5_RAT
 AC P14668;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88273202; PubMed=2968983;
 RA Pedinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K.,
 RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
 RA Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
 RA "Five distinct calcium and phospholipid binding proteins share
 RT homology with lipocortin I.";
 RL J. Biol. Chem. 263:10799-10811 (1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar;
 RX MEDLINE=96035863; PubMed=7556178;
 RA Imai Y., Kohsaka S.;
 RA "Structure of rat annexin V gene and molecular diversity of its
 RT transcripts.";
 RL Eur. J. Biochem. 232:327-334 (1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=93369587; PubMed=8362244;
 RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RA "Rat annexin V crystal structure: Ca(2+)-induced conformational
 RT changes.";
 RL Science 261:1321-1324 (1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC TISSUE=Kidney;
 RX MEDLINE=96069783; PubMed=7583670;
 RA Swaitio M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RA "Ca(2+)-bridging mechanism and phospholipid head group recognition in
 RT the membrane-binding protein annexin V.";
 RL Nat. Struct. Biol. 2:968-974 (1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
 RX MEDLINE=98272673; PubMed=9609693;
 RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swaitio M.A., Balch C.,
 RA Head J.F., Retzinger G., Dedman J.R., Seaton B.A.;
 RA "Mutational and crystallographic analyses of interfacial residues in
 RT annexin V suggest direct interactions with phospholipid membrane
 RT components.";
 RL Biochemistry 37:8004-8010 (1998).

RN [6]
 RP INTERACTION WITH DNMT1.
 RC STRAIN=Mistar; TISSUE=Brain;
 RX MEDLINE=96301899; PubMed=8667030;
 RA Onisawa K., Imai Y., Ito D., Kohsaka S.;
 RA "Molecular cloning and characterization of annexin V-binding protein
 RT with highly hydrophilic peptide structure.";
 RL J. Neurochem. 67:89-97 (1996).
 CC -1- FUNCTION: This protein is an anticoagulant protein that acts as
 CC indirect inhibitor of the thromboplastin-specific complex, which
 CC is involved in the blood coagulation cascade.
 CC -1- SUBUNIT: Monomer. Binds AFX and DNMT1.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M21730; AAA41512.1; -;
 DR EMBL; D42137; BAA07708.1; -;
 DR EMBL; D42129; BAA07708.1; JOINED.
 DR EMBL; D42130; BAA07708.1; JOINED.
 DR EMBL; D63337; BAA07708.1; JOINED.
 DR EMBL; D42132; BAA07708.1; JOINED.
 DR EMBL; D42131; BAA07708.1; JOINED.
 DR EMBL; D42133; BAA07708.1; JOINED.
 DR EMBL; D42134; BAA07708.1; JOINED.
 DR EMBL; D42135; BAA07708.1; JOINED.
 DR EMBL; D42136; BAA07708.1; JOINED.
 DR EMBL; D29250; LUR75.
 DR PIR; Z29250; LUR75.
 DR PDB; 2RAN; 30-NOV-94.
 DR PDB; 1A8A; 17-JUN-98.
 DR PDB; 1A8B; 17-JUN-98.
 DR PDB; 1BC0; 13-JAN-99.
 DR PDB; 1BC1; 13-JAN-99.
 DR PDB; 1BC3; 13-JAN-99.
 DR PDB; 1BCW; 13-JAN-99.
 DR PDB; 1BCY; 13-JAN-99.
 DR PDB; 1BCZ; 13-JAN-99.
 DR PDB; 1G5N; 13-MAR-02.
 DR PDB; 1N41; 04-FEB-03.
 DR PDB; 1N42; 04-FEB-03.
 DR PDB; 1N44; 04-FEB-03.
 DR PDB; 1N44; 04-FEB-03.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Placenta; Acetylation; 3D-structure.
 FT INT MET 0
 FT REPEAT 20 80 ANNEXIN 1.
 FT REPEAT 92 152 ANNEXIN 2.
 FT REPEAT 176 236 ANNEXIN 3.
 FT REPEAT 251 311 ANNEXIN 4.
 FT MOD RES 1 1 ACETYLATION.
 FT TURN 10 11
 FT HELIX 14 25
 FT HELIX 32 39
 FT TURN 40 41
 FT HELIX 44 58
 FT HELIX 62 69
 FT HELIX 72 82
 FT HELIX 85 97
 FT HELIX 104 113

FT HELIX 116 130
 FT HELIX 134 141
 FT HELIX 144 154
 FT TURN 155 156
 FT HELIX 166 179
 FT TURN 180 182
 FT HELIX 188 197
 FT HELIX 200 214
 FT HELIX 218 225
 FT HELIX 228 242
 FT HELIX 244 256
 FT HELIX 263 273
 FT TURN 274 277
 FT HELIX 278 289
 FT HELIX 293 300
 FT HELIX 303 313
 SQ SEQUENCE 318 AA, 35613 MW, 1A755A7C1FA1ICE CRC64;

Query Match 84.0%; Score 194; DB 1; Length 318;
 Best Local Similarity 79.2%; Pred. No. 2.9e-16;
 Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

1 RKAMKGLGTDSEIITLTLSRNSAORQETSAFKTLFGDLDLDDKSE 48
 22 RKAMKGLGTDSEIITLTLSRNSAORQETSAFKTLFGDLDLDDKSE 69

RESULT 6

ANX5_CYNPY STANDARD; PRT; 323 AA.
 AC P70075;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Yamamoto T., Hiko T., Abe S.I.;
 RT "Differential expression of annexin V during spermatogenesis in the
 newt *Cynops pyrrhogaster*.";
 RL Dev. Genes Evol. 206:64-71(1996).

-1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 membrane fusion and is involved in exocytosis (by similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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EMBL; D64134; BA01012.1; -
 DR HSSP; P06758; IAVH.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat.
 REPEAT 26 86 ANNEXIN 1.
 FT REPEAT 98 158 ANNEXIN 2.
 FT REPEAT 182 242 ANNEXIN 3.

FT REPEAT 257 317 ANNEXIN 4.
 SQ SEQUENCE 323 AA, 35981 MW, 044B31AC28164CE2 CRC64;
 Query Match 77.5%; Score 179; DB 1; Length 323;
 Best Local Similarity 75.0%; Pred. No. 1.9e-14;
 Matches 36; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

1 RKAMKGLGTDSEIITLTLSRNSAORQETSAFKTLFGDLDLDDKSE 48
 27 RKAMKGLGTDSEIITLTLSRNSAORQETSAFKTLFGDLDLDDKSE 74

RESULT 7

ANX4_BOVIN STANDARD; PRT; 318 AA.
 AC P13214;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (Protein X) (P32.5) (Placental anticoagulant protein II) (PAP-II)
 DE (P4-X) (35-Beta calcitriol) (Carbohydrate-binding protein P33/P41)
 DE (P33/41).
 GN ANX4 OR ANX4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=99050088; PubMed=2847715;
 RA Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
 RT "Cloning and characterization of a cDNA encoding bovine endonexin
 (chromobindin 4).";
 RL Biochem. Biophys. Res. Commun. 156:660-667(1988).

[2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96205957; PubMed=8631806;
 RA Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;
 RT "Characterization of carbohydrate-binding protein p33/41: relation
 RT with annexin IV, molecular basis of the doublet forms (p33 and p41),
 RT and modulation of the carbohydrate binding activity by
 RT phospholipids.";
 RL J. Biol. Chem. 271:7679-7685(1996).

[3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA Sutton R.B., Sprang S.R.;
 RL Submitted (SEP-1995) to the PDB data bank.
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RX MEDLINE=98070213; PubMed=9405281;
 RA Zanotti G., Malpegi G., Glubich F., Foll C., Stoppini M., Oliva L.,
 RA Savio A., Berni R.;
 RT "Structure of the trigonal crystal form of bovine annexin IV.";
 RL Biochem. J. 329:101-106(1998).

CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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EMBL; M22248; AAA30507.1; -

EMBL; X13627; CAA31954.1; -
 DR EMBL; D78178; BAA11243.1; -
 DR PIR; A31578; LUBO4.
 DR PDB; 1ANN; 29-JUN-96.
 DR PDB; 1AOM; 14-JAN-98.
 DR PDB; 114A; 25-APR-01.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR Prodom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 KW INIT MET
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 94 94 L -> V (IN REF. 2).
 FT CONFLICT 210 210 E -> K (IN REF. 2).
 FT HELIX 15 26
 FT HELIX 33 40
 FT TURN 41 42
 FT HELIX 45 59
 FT HELIX 63 70
 FT HELIX 73 83
 FT HELIX 86 98
 FT HELIX 105 114
 FT HELIX 117 131
 FT HELIX 135 142
 FT HELIX 145 155
 FT TURN 156 156
 FT TURN 162 162
 FT TURN 183 185
 FT HELIX 189 198
 FT HELIX 201 215
 FT HELIX 219 226
 FT HELIX 229 257
 FT HELIX 264 274
 FT TURN 275 278
 FT HELIX 279 290
 FT HELIX 294 301
 FT HELIX 304 314
 SQ SEQUENCE 318 AA; 35757 MW; 86BDBF349D774FD CRC64;
 Query Match 74.8%; Score 173; DB 1; Length 318;
 Best Local Similarity 70.8%; Pred. No. 1e-13; 8; Indels 0; Gaps 0;
 Matches 34; Conservative 6; Mismatches 0;
 QY 1 RKAMKGLGTDSEILTLTSSRNAROEISAQKTLFGRDLDDKSE 48
 Db 23 RKAMKGLGTDDEDAIIVLAVRSTAROEIRTAQKTTIGRDLMDLKE 70
 RESULT 8
 ANX4_PIG STANDARD; PRT; 318 AA.
 AC P08133; 029306;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV) (lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (Protein II) (P32.5) (Placental anticoagulant protein I) (PAI-II)
 DE (PP4-X) (35-beta calcimedlin).
 GN ANX4 OR ANX4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=96823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestinal epithelium;
 RX MEDLINE=87275850; PubMed=2956093;

FA Weber K., Johnson N., Plesmann U., Van P.N., Soling H.-D., Ampe C.
 RA Vanderkrogh J.;
 RT "The amino acid sequence of protein II and its phosphorylation site
 RT for protein kinase C; the domain structure Ca²⁺-modulated lipid
 RT binding proteins.";
 RL EMBO J. 6:1599-1604 (1987).
 RN [2]
 RP SEQUENCE OF 1-126 FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small
 RT library: analysis of 839 clones.";
 RL Mamm. Genome 7:509-517 (1996).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
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 CC
 DR EMBL; F14682; CAA23194.1; -
 DR PIR; A27107; LUPG4.
 DR HSSP; P13214; 1ANN.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR Prodom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
 KW Acetylation.
 FT INIT MET 0 0 ANNEXIN 1.
 FT REPEAT 22 82 ANNEXIN 2.
 FT REPEAT 94 154 ANNEXIN 3.
 FT REPEAT 178 238 ANNEXIN 4.
 FT REPEAT 253 313 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION (PROBABLE).
 FT MOD_RES 6 6 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 318 AA; 35697 MW; FA7D9CE2B76C31E8 CRC64;
 Query Match 74.5%; Score 172; DB 1; Length 318;
 Best Local Similarity 70.8%; Pred. No. 1.3e-13; 7; Indels 0; Gaps
 Matches 34; Conservative 7; Mismatches 7;
 QY 1 RKAMKGLGTDSEILTLTSSRNAROEISAQKTLFGRDLDDKSE 48
 Db 23 RKAMKGLGTDDEDAIIVLAVRSTAROEIRTAQKTTIGRDLMDLKE 70
 RESULT 9
 ANX6_BOVIN STANDARD; PRT; 618 AA.
 AC P79134;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
 DE (Fragment).
 GN ANX6 OR ANX6.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX Bovidae; Bovinae; Bos.
 RN [1] NCBI_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Camera C.; Creutz C.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=96422308; PubMed=9748523;
 RA Avila-Sakar A.J.; Creutz C.E.; Kretsinger R.H.;
 RL "Crystal structure of bovine annexin VI in a calcium-bound state";
 Biochim. Biophys. Acta 1387:103-116(1998).
 CC -!- FUNCTION: May associate with CD21. May regulate the release of
 Ca(2+) from intracellular stores.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.
 CC -!- PTM: Phosphorylated in response to growth factor stimulation (By
 similarity).
 CC -!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -!- SIMILARITY: Belongs to the annexin family.
 CC -!- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; U87539; AAB47570.1; -.
 DR PDB; 1AVC; 28-JAN-98.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin.8.
 DR PRINTS; PR00196; ANNEXIN.
 DR PRODOM; PD000143; Annexin; 8.
 DR SMART; SM00335; ANX; 8.
 DR PROSITE; PS00223; ANNEXIN; 6.
 DR Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
 KM 3D-structure.
 FT NON_TER 1 1
 FT REPEAT <1 34 ANNEXIN 1.
 FT REPEAT 46 106 ANNEXIN 2.
 FT REPEAT 130 190 ANNEXIN 3.
 FT REPEAT 205 265 ANNEXIN 4.
 FT REPEAT 317 377 ANNEXIN 5.
 FT REPEAT 389 449 ANNEXIN 6.
 FT REPEAT 478 538 ANNEXIN 7.
 FT REPEAT 553 613 ANNEXIN 8.
 FT HELIX 1 11
 FT HELIX 15 22
 FT HELIX 26 35
 FT HELIX 38 50
 FT HELIX 57 66
 FT HELIX 69 83
 FT HELIX 87 92
 FT TURN 93 94
 FT TURN 97 97
 FT HELIX 98 108
 FT TURN 119 132
 FT TURN 133 135
 FT HELIX 141 150
 FT HELIX 153 167
 FT HELIX 171 175
 FT HELIX 176 177
 FT HELIX 181 195
 FT HELIX 197 209
 FT HELIX 216 225
 FT TURN 226 230
 FT HELIX 231 241
 FT HELIX 246 253

FT HELIX 256 266
 FT HELIX 278 293
 FT TURN 306 307
 FT HELIX 310 319
 FT TURN 320 321
 FT HELIX 328 335
 FT TURN 336 337
 FT HELIX 340 354
 FT HELIX 358 365
 FT HELIX 368 378
 FT HELIX 381 392
 FT TURN 393 393
 FT HELIX 400 407
 FT TURN 408 409
 FT HELIX 412 425
 FT HELIX 430 437
 FT HELIX 440 449
 FT TURN 450 451
 FT HELIX 461 474
 FT HELIX 491 498
 FT HELIX 501 515
 FT HELIX 519 526
 FT HELIX 529 556
 FT TURN 557 557
 FT HELIX 564 573
 FT TURN 574 578
 FT HELIX 579 590
 FT HELIX 594 601
 FT HELIX 604 614
 FT TURN 615 615
 SQ SEQUENCE 618 AA; 69796 MW; 5571F70F24B5836F CRC64;

Query Match 73.6%; Score 170; DB 1; Length 618;
 Best Local Similarity 68.8%; Pred. No. 4.6e-13;
 Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDSEILTLTSRSNAQROEISAFTLFGRLDLDLXSE 48
 Db 318 RKAMKGLGTDSEITLITLTSRSNAQROEISAFTLFGRLDLDLXSE 365

RESULT 10
 ANX7_MOUSE STANDARD; PRT; 463 AA.
 AC 007076;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A7 (Annexin VII) (Synexin).
 GN ANX7 OR ANX7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93168121; PubMed=7916616;
 RA Zhang-Keck Z.Y.; Burns A.L.; Pollard H.B.;
 RT "Mouse synexin (annexin VII) polymorphisms and a phylogenetic
 comparison with other synexins.";
 RL Biochem. J. 289:735-741(1993).
 CC -!- FUNCTION: Calcium/phospholipid-binding protein which promotes
 membrane fusion and is involved in exocytosis.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.
 CC -!- SIMILARITY: Belongs to the annexin family.
 CC -!- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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CC EMBL; L13129; AAA37238.1; -
 CC HSSP; P26256; 1DM5.
 DR MGD; MG1:8031; ANX4.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat.
 FT DOMAIN 1 143 REPEAT-RICH REGION.
 FT REPEAT 169 229 ANNEXIN 1.
 FT REPEAT 241 301 ANNEXIN 2.
 FT REPEAT 324 384 ANNEXIN 3.
 FT REPEAT 400 460 ANNEXIN 4.
 FT DOMAIN 5 20 3 X 5 AA TANDEM REPEATS OF G-Y-P-P-X.
 FT REPEAT 5 9 1.
 FT REPEAT 10 14 2.
 FT REPEAT 16 20 3.
 SQ SEQUENCE 463 AA; 49939 MW; 50F7B20FD48EBDC5 CRC64;

Query Match 73.2%; Score 169; DB 1; Length 463;
 Best Local Similarity 64.6%; Pred. No. 4, 5e-13;
 Matches 31; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

1 RKAMGIGTDEESITLTLSRSGAQRSEIAFKTLFGRLDLDKSE 48
 170 RKAMGIGTDEGATVAVNSRNDORQIKAFKTMGKDLKDKSE 217

RESULT 11

ANX4_HUMAN STANDARD; PRT; 318 AA.
 AC P09525; O96F33; O9BWK1;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (Pp4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/41).
 DE ANX4 OR ANX4.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8309022; PubMed=2970257;
 RA Grundmann U., Aumann E., Abel K.-J., Kuepper H.A.;
 RT "Isolation and expression of cDNA coding for a new member of the phospholipase A2 inhibitor family."
 RL Behring Inst. Mitt. 82:59-67(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92155721; PubMed=1346776;
 RA Tait J.F., Smith C., Frankenherry D.A., Miao C.H., Adler D.A.,
 RT "Chromosomal mapping of the human annexin IV (ANX4) gene";
 RL Genomics 12:313-318(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97239215; PubMed=9084877;
 RA Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
 RT "Characterization of human p33/41 (annexin IV), a Ca²⁺ dependent carbohydrate-binding protein with monoclonal anti-annexin IV antibodies, A511 and A517."
 RL Biol. Pharm. Bull. 20:224-229(1997).
 RN [4]

RP SEQUENCE FROM N.A.
 RC TISSUE=Eye, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Shevchenko Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 26-55; 98-123 AND 279-307.
 RX MEDLINE=8906652; PubMed=2974032;
 RA Ahn N.G., Teller D.C., Bilenkowski M.J., McMullen B.A., Lipkin E.W.,
 RA de Haen C.;
 RT "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor."
 RL J. Biol. Chem. 263:18657-18663(1988).
 RN [6]
 RP SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
 RX MEDLINE=89118212; PubMed=2975506;
 RA Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
 RA Hendrickson L.E., Fujikawa K.;
 RT "Placental anticoagulant proteins: Isolation and comparative characterization four members of the lipocortin family."
 RL Biochemistry 27:6268-6276(1988).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=91073383; PubMed=2254922;
 RA Freemont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;
 RT "Crystallization and preliminary X-ray crystallographic studies of human placental annexin IV."
 RL J. Mol. Biol. 216:219-221(1990).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
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CC EMBL; M19383; AAC41689.1; ALT_INIT.
 DR EMBL; M82809; AAA51740.1; -
 DR EMBL; D78152; BAA11227.1; ALT_INIT.
 DR EMBL; BC00182; AAH00182.1; ALT_INIT.
 DR EMBL; BC011659; AAH11659.1; ALT_INIT.
 DR PIR; A42077; A42077.
 DR HSSP; P13214; 1ANN.
 DR SWISS-2DPAGE; P09525; HUMAN.
 DR PMAA-2DPAGE; P09525; -
 DR Genew; HGNC:542; ANX4.

SEQUENCE FROM N.A.
TISSUE=Uterus;

FT	INIT_MET	0	0	ANNEXIN 1.
FT	REPEAT	28	88	ANNEXIN 1.
FT	REPEAT	100	160	ANNEXIN 2.
FT	REPEAT	184	244	ANNEXIN 3.
FT	REPEAT	259	319	ANNEXIN 4.
FT	REPEAT	371	431	ANNEXIN 5.
FT	REPEAT	443	503	ANNEXIN 6.
FT	REPEAT	532	592	ANNEXIN 7.
FT	REPEAT	607	667	ANNEXIN 8.
FT	MOD_RES	1	1	ACTIVATION

FT CONFLICT 225 226 IE -> MK (IN REF. 2).
FT CONFLICT 554 554 S -> T (IN REF. 2).
FT CONFLICT 618 618 E -> D (IN REF. 1).
SQ SEQUENCE 672 AA; 75742 MW; 2829237029BDIDCB CRC64;

Query Match 72.3%; Score 167; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 1.2e-12;
Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 RKAMKGLGDEBSILTLTSSNAQROEISAAPKTLFGRLDLDLXSE 48
Db 372 RKAMKGLGDEBSILTLTSSNAQROEISAAPKTLFGRLDLDLXSE 419

RESULT 13

ANK6_CHICK STANDARD; PRT; 671 AA.

AC P51901;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A6 (Annexin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
GN ANX6 OR ANX6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RX MEDLINE=94092130; PubMed=8267590;
RA Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthier R.E.;
RT "Characterization, cloning and expression of the 67-kDa annexin from
RT chicken growth plate cartilage matrix vesicles."
RL Biochem. Biophys. Res. Commun. 197:556-561(1993).
CC -1- FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 8 annexin repeats.
CC
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CC
CC EMBL; S67466; AAB29337.2; -
DR PIR; JC2029; JC2029.
DR HSSP; P79134; IAVC.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin. 8.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin. 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 5.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT REPEAT 27 87 ANNEXIN 1.
FT REPEAT 99 159 ANNEXIN 2.
FT REPEAT 183 243 ANNEXIN 3.
FT REPEAT 258 318 ANNEXIN 4.
FT REPEAT 370 430 ANNEXIN 5.
FT REPEAT 442 502 ANNEXIN 6.
FT REPEAT 531 592 ANNEXIN 7.
FT REPEAT 607 666 ANNEXIN 8.
SQ SEQUENCE 671 AA; 75218 MW; D0E02F4311A93D98 CRC64;

Query Match 71.9%; Score 166; DB 1; Length 671;
Best Local Similarity 70.8%; Pred. No. 1.5e-12;

Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps

Qy 1 RKAMKGLGDEBSILTLTSSNAQROEISAAPKTLFGRLDLDLXSE 48
Db 371 RKAMKGLGDEBSILTLTSSNAQROEISAAPKTLFGRLDLDLXSE 418

RESULT 14

ANK4_CANFA STANDARD; PRT; 318 AA.

AC P50994;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule
DE membrane associated protein) (ZAP36).
GN ANX4 OR ANX4.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
ON NCBI_TaxID=9615;
RX MEDLINE=22015264; PubMed=12020832;
RA Fukuda S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.;
RT "Cloning and characterization of ZAP36, an annexin-like, zymogen
RT granule membrane associated protein, in exocrine pancreas."
RL Biochim. Biophys. Acta 1575:148-152(2002).
RN [2]
RX MEDLINE=94362286; PubMed=7765250;
RA Fukuda S.-I.;
RT "Analysis of ZAPs, zymogen granule membrane associated proteins, in
RT the regulated exocytosis of the pancreas."
RL Biosci. Biotechnol. Biochem. 58:1282-1285(1994).
CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
CC membrane fusion and is involved in exocytosis (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
CC (By similarity).
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D38223; BAA07398.1; -
DR HSSP; P13214; IANN.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin. 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin. 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INIT MET 0
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
FT CONFLICT 138 138 V -> D (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 318 AA; 35681 MW; 42EFSB8917984863 CRC64;

Query Match 71.4%; Score 165; DB 1; Length 318;
Best Local Similarity 64.6%; Pred. No. 9.5e-13;
Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps

OY 1 RKAMKGLGDEESILTLTSSNAQROEISAAPKTLFGRLDLDLXSE 48
 DB 23 RKAMKGLGDEDAIISVLAAPRNTSQROEIRYAKSTIGRLDMDLXSE 70

Search completed: April 8, 2004, 11:57:13
 Job time : 11 secs

RESULT 15

ANX6_MOUSE STANDARD; PRT; 672 AA.

AC P14824;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANXA6 OR ANX6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;
 RX MEDLINE=89010687; PubMed=2972541;
 RA Moss S.E., Crumpton M.R., Crumpton M.J.;
 RT "Molecular cloning of murine p68, a Ca2+-binding protein of the
 RT lipocortin family."
 RL Eur. J. Biochem. 177:21-27 (1988).

CC -!- FUNCTION: May associate with CD21. May regulate the release of
 Ca(2+) from intracellular stores.

CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.

CC -!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 -!- SIMILARITY: Belongs to the annexin family.

CC -!- SIMILARITY: Contains 8 annexin repeats.

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 CC -----

DR EMBL: X13460; CAJ31808.1; -.
 DR PIR: S01786; S01786.

DR HSSP: P79134; IAVC.

DR MGD: MGI:88255; Anxa6.

DR InterPro: IPR001464; Annexin.

DR Pfam: PF00191; annexin; 8.

DR PRINTS: PR00196; ANNEXIN.

DR ProDom: PD000143; Annexin; 8.

DR SMART: SM00335; ANX; 8.

DR PROSITE: PS00223; ANNEXIN; 8.
 DR Annexin; Calcium/phospholipid-binding; Repeat.

FT INIT_MET 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 SQ SEQUENCE 672 AA; 75755 MW; 2D85C11DD235FC76 CRC64;

Query Match 71.0%; Score 164; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 2.7e-12;

Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 1 RKAMKGLGDEESILTLTSSNAQROEISAAPKTLFGRLDLDLXSE 48
 DB 372 RKAMKGLGDEDAIISVLAAPRNTSQROEIRYAKSTIGRLDMDLXSE 419

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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:18:15 ; Search time 55 Seconds
(without alignments)
246.587 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72
Perfect score: 231
Sequence: 1 RKAMKGLGDEESILTLITS.....ISAPFTLFGRLDLDKSE 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq_29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	231	100.0	117	6	ABU00010 Human nov
2	231	100.0	146	2	AAR13592 PAP-I-pro
3	231	100.0	208	3	AAB58393 lung canc
4	231	100.0	319	2	AAR26276 CFB-I. 3/
5	231	100.0	319	2	AAR26180 CFB-I. 3/
6	231	100.0	319	2	AAR41021 Calphobin
7	231	100.0	319	5	ABG32550 Human CPB
8	231	100.0	319	7	ADBS5088 Human pro
9	231	100.0	319	7	ADBS5187 Human pro
10	231	100.0	320	1	AAP82317 PAP-I iso
11	231	100.0	320	1	AAP80511 Placentat
12	231	100.0	320	1	AAP80242 Sequence
13	231	100.0	320	1	AAP90053 anticocu
14	231	100.0	320	1	AAP91363 Human lip
15	231	100.0	320	1	AAP91363 Human lip
16	231	100.0	320	2	AAR13082 PAP-I. 3/
17	231	100.0	320	2	AAR11910 Vascular
18	231	100.0	320	2	AAY13923 S65T GFP
19	231	100.0	320	3	AAY84788 Amino aci
20	231	100.0	320	5	ABG31220 Human ann
21	231	100.0	327	4	AAB50864 Modified
22	231	100.0	327	4	AAB50865 Modified
23	231	100.0	327	4	AAB50863 Modified
24	231	100.0	509	2	AAR13083 PAP-I-pro
25	231	100.0	600	3	AAY92930 Annexin V

26	228	98.7	320	1	AAP80714
27	223	96.5	319	2	AAR25718
28	207	89.6	319	2	AAY13924
29	207	89.6	319	5	ABBS7067
30	206	89.2	313	6	ABG74925
31	206	89.2	321	6	ABG74924
32	194	84.0	302	7	ADBS5086
33	194	84.0	318	2	AAY13925
34	194	84.0	319	2	ADBS5185
35	194	84.0	319	2	AAR75695
36	194	84.0	319	6	ABP56248
37	194	84.0	659	6	ABP56249
38	169	73.2	463	7	ADD47587
39	167	72.3	299	5	ABP69394
40	167	72.3	299	6	ABR43299
41	167	72.3	318	7	ADBS1027
42	167	72.3	320	7	AAY84790
43	167	72.3	321	1	AAP91913
44	167	72.3	321	2	AAY13926
45	167	72.3	321	5	ABG96279

ALIGNMENTS

RESULT 1	ABU00010	standard, protein, 117 AA.
ID	ABU00010	
XX	ABU00010;	
AC	17-JAN-2003 (first entry)	
DT		
XX		
DE	Human novel polypeptide #103.	
XX		
XX	Human; genetic disorder; gene mapping; medical imaging; cancer;	
KW	neurodegenerative disorder; lymphoid cell disorder; osteoporosis;	
KW	Parkinson's disease; Alzheimer's disease; bone degenerative disorder;	
KW	osteoarthritis; periodontal disease; liver fibrosis; viral infection;	
KW	fungal infection; bacterial infection; autoimmune disease; diabetes;	
KW	atopic dermatitis.	
OS	Homo sapiens.	
PN	WO200274961-A1.	
XX		
PD	26-SEP-2002.	
XX		
PF	14-MAR-2002; 2002WO-US005109.	
XX		
PR	15-MAR-2001; 2001US-00810173.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren	
PI	Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,	
PI	Wehrman T, Wang J, Wang D, Dimaacac RT;	
XX		
DR	WPI: 2003-040556/03.	
DR	N-PSDB; ABBX05086.	
XX		
XX	New isolated polypeptides and polynucleotides, useful for preventin	
PT	treatin or ameliorating medical conditions, such as cancer.	
PT	neurodegenerative disorders, lymphoid cell disorders, bone degenera	
PT	disorders, and infections.	
PS		
PS	Claim 9, SEQ ID NO 629; 235pp; English.	
XX		
XX	The invention relates to human polynucleotides and the polypeptides	
CC	encode. The polynucleotides and polypeptides are useful in diagnosi	
CC	forensics, gene mapping, medical imaging, identification of mutatio	
CC	responsible for genetic disorders or other traits, assessing biologi	
CC	and producing many other types of data and products dependent on DN	

AAP80714	Sequen
AAR25718	CPB-I
AAY13924	S65T G
ABBS7067	Mouse
ABG74925	Chicken
ABG74924	Chicken
ADBS5086	Rat P
ADBS5185	Rat P
AAR75695	Rat at
ABP56248	Human
ABP56249	Modif
ADD47587	Rat P
ABP69394	Human
ABR43299	Human
ADBS1027	Amino
AAY84790	Antic
AAP91913	Antic
AAY13926	S65T
ABG96279	Human

CC amino acid sequences. They are also useful for preventing, treating or
CC ameliorating medical conditions, such as cancer, neurodegenerative
CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,
CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or
CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).
CC Sequences ABG9888-ABG9989 and ABU0010-ABU0043 represent human
CC polypeptides of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office
XX

Sequence 117 AA;

Query Match 100.0%; Score 231; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESITLTLSRSNAQROEISAFTLFGRLDLDKSE 48
DB 25 RKAMKGLTDEESITLTLSRSNAQROEISAFTLFGRLDLDKSE 72

RESULT 2

AA13592 standard; protein, 146 AA.

AA13592;

25-MAR-2003 (revised)
30-SEP-1991 (first entry)

PAP-I-protein C fusion construct.

Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP,
gla-domain; VKDP.

Homo sapiens.

Location/Qualifiers
1..136
/label= PAP-I

Protein
137..140
/label= protein C
/note= "amino acids 46-49"

Misc-difference 141..146
/label= LYS, ARG

MO9109953-A.

11-JUL-1991.

29-DEC-1989; 89US-00459082.

29-DEC-1989; 89US-00459082.

(ZYMO) ZYMOGENETICS INC.

Foster DC;

WPI, 1991-222905/30.

N-PSDB; AAQ12681.

Recombinant prodn. of hybrid phospholipid-binding proteins - comprising
lipocortin phospholipid-binding domain and vitamin-K-dependent protein.

Claim 21; Page 41; 57pp; English.

The fusion was constructed using site-directed mutagenesis to fuse PAP-I
encoding amino acid 1-136 with a protein C DNA sequence at the codon for
amino acid 46. A plasmid contg. this construct was transfected into BHK
cells which were then cultured to produce PAP-I-protein C fusions which
were activated to a form fully active in both amidolytic and

CC anticoagulant assays. This sequence contains and additional fragment of
CC amino acids Lys or Arg, between the light and heavy chains. At least
CC three amino acids are present. See also AAQ12678-81. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX

Sequence 146 AA;

Query Match 100.0%; Score 231; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESITLTLSRSNAQROEISAFTLFGRLDLDKSE 48
DB 24 RKAMKGLTDEESITLTLSRSNAQROEISAFTLFGRLDLDKSE 71

RESULT 3

AA58393 standard; protein, 208 AA.

AA58393;

14-MAR-2001 (first entry)

Lung cancer associated polypeptide sequence SEQ ID 731.

Human; lung cancer associated protein; neuroprotective; cytosolic;
cardioactive; immunomodulatory; muscular active; vulnerable;
gastrointestinal; nephrotoxic; anti-infective; gynecological;
antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
proliferative disorder; wound healing; infectious disease.

Homo sapiens.

MO20005180-A2.

21-SEP-2000.

08-MAR-2000; 2000WO-US005918.

12-MAR-1999; 99US-0124270P.

(HUMA-) HUMAN GENOME SCI INC.

(ROSE/) ROSEN C A.

Ruben SM;

WPI; 2000-587514/55.

N-PSDB; AAF18269.

Lung cancer associated gene sequences, referred to as lung cancer
antigens, useful for treatment, prevention, and diagnosis of disorders
such as lung cancer.

Claim 11; Page 1248-1249; 1425pp; English.

Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
associated proteins represented in AAB58106 - AAB58548. Lung cancer
associated proteins and polynucleotide sequences, their agonists, and
antagonists may have neuroprotective, cytosolic, cardioactive;
immunomodulatory; muscular active general; vulnerable; gastrointestinal
general; nephrotoxic; anti-infective; gynecological; or antibacterial
activity. The invention also includes antibodies specific for the protein
or polynucleotide sequences. The lung cancer associated polynucleotide
sequences may be used for detection of lung cancer, chromosome
identification, as chromosome markers, and for numerous other diagnostic
or research purposes. The proteins may be used to treat disorders such as
neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
cardiovascular, renal, and proliferative disorders. The proteins may also
be used in the treatment of wounds and infectious diseases.
Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
used in the course of the invention for the identification and
characterisation of the polynucleotide and protein sequences

XX Sequence 208 AA;

Query Match 100.0%; Score 231; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGRLDDPKSE 48
28 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGRLDDPKSE 75

RESULT 4
AAR26276
ID AAR26276 standard; protein; 319 AA.

AC AAR26276;
DT 10-MAR-2003 (revised)
DT 04-FEB-1993 (first entry)

DE CPB-I.
KW CPB-I; stabilisation; frozen; molten; processed; activity.

OS Homo sapiens.

PN JP04198195-A.

PD 17-JUL-1992.

PF 28-NOV-1990; 90JP-00328286.

PR 28-NOV-1990; 90JP-00328286.

PA (KOMA) KOMA CO LTD.

PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.

DR WPI; 1992-288937/35.

XX Stabilisation of CPB-I for drug compsn. - by adding basic aminoacid
PT selected from lysine, arginine and/or ornithine.

PS Disclosure; Page 2; 4pp; Japanese.

CC The sequence given is the amino acid sequence of CPB-I. CPB-I was used
CC within a method which involved adding basic amino acids to it which
CC resulted in its stabilisation. This lead to the production of CPB-I which
CC keeps its activity when it is frozen, molten or has been processed by
CC several procedures. (Updated on 10-MAR-2003 to add missing OS field.)

SQ Sequence 319 AA;

Query Match 100.0%; Score 231; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGRLDDPKSE 48
24 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGRLDDPKSE 71

RESULT 5
AAR26180
ID AAR26180 standard; protein; 319 AA.

AC AAR26180;

DT 10-MAR-2003 (revised)

DT 04-FEB-1993 (first entry)

DE CPB-I.

KW CPB-I; saccharides; stabilisation; antihemagglutination; dermal disease.

OS Homo sapiens.

PN JP04198196-A.

PD 17-JUL-1992.

PF 28-NOV-1990; 90JP-00328287.

PR 28-NOV-1990; 90JP-00328287.

PA (KOMA) KOMA CO LTD.

PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.

DR WPI; 1992-288938/35.

XX Stabilisation of CPB-I for drug compsn. - contains saccharide select
PT from glucose, glucosamine, xylose, saccharose and/or dextran.

PS Disclosure; Page 2; 4pp; Japanese.

CC The sequence given is the amino acid sequence of CPB-I. CPB-I was used
CC within the method of the invention which involved adding saccharides
CC it which resulted in its stabilisation. The saccharide was pref. glu
CC glucosamine, xylose, saccharose, or dextran. This lead to the product
CC of CPB-I which kept its activity when it had been processed by sever
CC treatments. CPB-I can be used as a medicine for antihemagglutination
CC dermal and corneal diseases. (Updated on 10-MAR-2003 to add missing
CC field.)

SQ Sequence 319 AA;

Query Match 100.0%; Score 231; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGRLDDPKSE 48
24 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGRLDDPKSE 71

RESULT 6
AAR41021
ID AAR41021 standard; protein; 319 AA.

AC AAR41021;

DT 29-MAR-1994 (first entry)

DE Calphobindin I (CPB-I).

KW Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.

OS Homo sapiens.

PN JP05213769-A.

PD 24-AUG-1993.

PF 04-FEB-1992; 92JP-00019032.

PR 04-FEB-1992; 92JP-00019032.

PA (KOMA) KOMA CO LTD.

PA (KAGA) ZH KAGAKU OYOBI KESSEN RYOHO KENKITSUHO.

DR WPI; 1993-299558/38.

XX Protein kinase C inhibitor effective against malignant tumours - cc
PT (opt. recombinant) calphobindin I.

PS Claim 1; Page 2-3; 6pp; Japanese.

CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I) inhibits
CC protein kinase C (PKC) and is useful in the treatment of malignant
CC tumours caused by abnormal activation of PKC. CPB-I is extracted from
CC human or animal organs and may be applied intravenously, orally,
CC intramuscularly, percutaneously or rectally.

XX Sequence 319 AA;

Query Match 100.0%; Score 231; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESILTLTTRSNAPORISAFKTLFGEDLDDKSE 48
DB 24 RKAMKGLTDEESILTLTTRSNAPORISAFKTLFGEDLDDKSE 71

RESULT 7
ABG32550
ID ABG32550 standard; protein; 319 AA.

XX ABG32550;

XX 29-NOV-2002 (first entry)

XX Human CPB-1 protein.

XX Human; CPB-I, eye drop; ophthalmological; anexin V; corneal disease;
XX calcium/phospholipid binding protein; polyhydric alcohol.

XX Homo sapiens.

XX WO200267977-A1.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-JP001563.

XX 26-FEB-2001; 2001JP-00050297.

XX (KOMA) KOMA CO LTD.

XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX Naruse H, Sano M, Shinoda Y, Inagi T;

XX WPI; 2002-674988/72.

XX Eye drops for treating e.g. corneal diseases, contain CPB-I and
XX polyhydric alcohol with specific carbonyl value, without unpleasant
XX irritation upon dropping but with satisfactory long-term storability.

XX Disclosure; Page 13-14; 16pp; Japanese.

XX The invention relates to eye drops contain CPB-I (anexin V) and a
XX polyhydric alcohol having a carbonyl value of not more than 5micro
XX Mol/9. The eyes drops are for treating e.g. corneal diseases. Such eye
XX drops are without unpleasant irritation upon dropping but with
XX satisfactory long-term storage stability. The present sequence is the
XX human CPB-I (calcium/phospholipid binding) protein

XX Sequence 319 AA;

Query Match 100.0%; Score 231; DB 5; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESILTLTTRSNAPORISAFKTLFGEDLDDKSE 48
DB 24 RKAMKGLTDEESILTLTTRSNAPORISAFKTLFGEDLDDKSE 71

RESULT 8
ADE55088
ID ADE55088 standard; protein; 319 AA.

XX ADE55088;

XX 29-JAN-2004 (first entry)

XX Human Protein P08758, SEQ ID NO 893.

XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P08758.

XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
XX injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 319 AA;

Query Match 100.0%; Score 231; DB 7; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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XX AC AAP80511;
XX DT 25-MAR-2003 (revised)
XX DT 10-MAR-2003 (revised)
XX DT 12-NOV-1990 (first entry)
XX DE Placental coagulation inhibitor.
XX KM Placental coagulation inhibitor; disseminated vascular coagulation;
XX KM thrombosis.
XX OS Homo sapiens.
XX PN EP279459-A.
XX PD 24-AUG-1988.
XX PF 19-FEB-1988; 88EP-00102468.
XX PR 20-FEB-1987; 87JP-00037227.
XX PR 23-JUL-1987; 87JP-00184428.
XX PA (KOMA ) KOMA CO LTD.
XX PI Saino Y, Iwasaki A, Suda M,
XX DR WPI; 1988-236733/34.
XX DR N-PSDB; AAN81113.
XX PT Recombinant placental coagulation inhibitor - useful for the prevention
XX PT and treatment of thromboses or disseminated intravascular coagulation.
XX PS Disclosure; Page 7; 31pp; English.
XX SS
XX CC This polypeptide exhibits strong anticoagulant activities and is useful
XX CC for the treatment and prevention of e.g. thrombosis or disseminated
XX CC intravascular coagulation in the brain, heart and peripheral blood
XX CC vessels, such as cerebral and myocardial infarction. It has no
XX CC antigenicity against man and can be produced in large amts. using
XX CC recombinant methods. (Updated on 10-MAR-2003 to add missing OG field.)
XX CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX SQ
XX Sequence 320 AA;

Query Match
Best Local Similarity 100.0%; Score 231; DB 1; Length 320;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAAMGGLGTDESIILTLTSSNAQROETSAAFKTLFGRLDDDKSE 48
DB 25 RKAAMGGLGTDESIILTLTSSNAQROETSAAFKTLFGRLDDDKSE 72

RESULT 12
AAP80242
ID AAP80242 standard; protein; 320 AA.
XX AC AAP80242;
XX DT 25-MAR-2003 (revised)
XX DT 12-SEP-1990 (first entry)
XX DE Sequence vascular anticoagulating protein (VAP) VAC-alpha (asp22).
XX KM Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
XX KM antiinflammatory; phospholipase inhibitor.
XX OS Homo sapiens.
XX PN W08807576-A.
XX

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PD 06-OCT-1988.
XX PF 26-MAR-1988; 88WO-EP000266.
XX PR 28-MAR-1987; 87DE-03710309.
XX PR 28-MAR-1987; 87DE-03710364.
XX PR 28-MAR-1987; 87DE-03710430.
XX PR 04-NOV-1987; 87DE-03737367.
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX PI Hauptmann R, Maurexfoxy I, Bodo G, Sweetly P, Stratowa C;
XX PI Falkner E, Adole G, Reutlingsp CMP;
XX DR WPI; 1988-292861/41.
XX DR N-PSDB; AAN80872.
XX PT New vascular anti-coagulating proteins - useful as thrombin inhibitors,
XX PT antiinflammatory agents, etc.
XX PS Claim 41; Page 171-72; 183pp; German.
XX CC The DNA is produced by determining the amino acid sequence of isolated
XX CC and highly purified VAPs, constructing DNA probes on the basis of this
XX CC sequence, using the probes to search through suitable cDNA libraries,
XX CC isolating cDNA that hybridises with the probes, by inserting the cDNA
XX CC into a suitable vector, and using the vector to transform a host
XX CC organism. VAC-alpha has anticoagulant activity under certain conditions,
XX CC but loses this activity in the event of severe bleeding. It acts by
XX CC inhibiting conversion of factor X to factor Xa and conversion of
XX CC prothrombin to thrombin. It is structurally related to lipocortin I
XX CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
XX CC has similar antiinflammatory and phospholipase inhibitory activity.
XX CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
XX CC correct PA field.)
XX SQ
XX Sequence 320 AA;

Query Match
Best Local Similarity 100.0%; Score 231; DB 1; Length 320;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAAMGGLGTDESIILTLTSSNAQROETSAAFKTLFGRLDDDKSE 48
DB 25 RKAAMGGLGTDESIILTLTSSNAQROETSAAFKTLFGRLDDDKSE 72

RESULT 13
AAP90053
ID AAP90053 standard; protein; 320 AA.
XX AC AAP90053;
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 01-NOV-1989 (first entry)
XX DE anticoagulant PP4 protein.
XX KM Anticoagulant; PP4 protein; thromboplastin.
XX OS Homo sapiens; (human).
XX PN EP318703-A.
XX PD 07-JUN-1989.
XX PF 29-OCT-1988; 88EP-00118039.
XX PR 03-NOV-1987; 87DE-03737239.
XX PA (BEHM ) BEHRINGER AG.
XX

```

PI Grundmann U, Abel KU, Kupper H;
XX
DR WPI; 1989-166767/23.
XX
PT New DNA sequence encoding anticoagulant P4 protein - and new recombinant
PT protein, vectors, antibodies, etc., useful therapeutically and
PT diagnostically.
XX
PS Claim 1; Page 11 and Table 1; 12pp; German.
XX
XX Amino acid sequence of anticoagulant P4 protein. This inhibits blood
CC coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 320 AA;
Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKAMKGLGTDSESLITLTSRSNAQROEISAFAKTLFGRLDLDKSE 48
DB 25 RKAMKGLGTDSESLITLTSRSNAQROEISAFAKTLFGRLDLDKSE 72
RESULT 14
AAP91363
ID AAP91363 standard; protein; 320 AA.
XX
AC AAP91363;
XX
DT 22-DEC-1989 (first entry)
XX
DE Human lipocortin-V.
XX
KM Human lipocortin-V; lambdaHLipo V-1; anti-inflammatory agent.
XX
OS Homo sapiens.
XX
PN EP30396-A.
XX
PD 30-AUG-1989.
XX
PF 20-FEB-1989; 89BP-00301603.
XX
PR 26-FEB-1988; 88US-00160866.
XX
PA (BIO) BIOGEN INC.
XX
PA (BIO) BIOGEN INC.
XX
PI Wallner BP, Pepinsky RB, Browning JL;
XX
DR WPI; 1989-250486/35.
XX
PT Human lipocortin cpds. III, IV, V, and VI - used in treatment of
PT arthritic, allergic, dermatologic, ophthalmic and collagen disorders
PT involving inflammatory processes.
XX
PS Claim 16; Fig 4; 32pp; English.
XX
XX Human lipocortin-V was isolated from a lambda gt10 human peripheral blood
CC lymphocyte cDNA library with rat lipocortin-V cDNA of lambda Rlipo V-1 as
CC probe. Lipocortins are anti-inflammatory agents and can be used to treat
CC arthritic, allergic, dermatologic, ophthalmic, and collagen diseases. See
CC also AAN90598, AAN90599, and AAP91362
XX
SQ Sequence 320 AA;
Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDSESLITLTSRSNAQROEISAFAKTLFGRLDLDKSE 48
DB 25 RKAMKGLGTDSESLITLTSRSNAQROEISAFAKTLFGRLDLDKSE 72
RESULT 15
AAP91953
ID AAP91953 standard; protein; 320 AA.
XX
AC AAP91953;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 30-JUL-1989 (first entry)
XX
DE Vascular anti-coagulating protein-alpha.
XX
KM Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
PN DE3810331-A.
XX
PD 05-OCT-1989.
XX
PF 26-MAR-1988; 88DE-03810331.
XX
PR 26-MAR-1988; 88DE-03810331.
XX
PA (BOEH) BOEHRINGER INGELHEIM.
XX
PI Gunther A;
XX
DR WPI; 1989-293724/41.
DR N-PSDB; AAN91353.
XX
PT Monoclonal antibodies to vascular anti-coagulating proteins - and
PT hybridomas producing such antibodies.
XX
PS Disclosure; Fig 1; 11pp; German.
XX
XX This vascular anti-coagulating protein (VAC)-alpha is used in the
CC preparation of monoclonal antibodies (mAbs). The VAC-alpha is injected
CC into a host animal, in conjugation with eg keyhole limpet haemocyanin
CC and the B-cells from immunised hosts are then fused with myeloma ce
CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to
CC alpha. Abs can be used as immunoassay reagents to detect VAC protei
CC affinity ligands for protein purification, and as medicaments for bindi
CC and/or neutralising VAC proteins in vivo. See also AAN91354 and BP-
CC 181465. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardi
CC field)
XX
SQ Sequence 320 AA;
Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKAMKGLGTDSESLITLTSRSNAQROEISAFAKTLFGRLDLDKSE 48
DB 25 RKAMKGLGTDSESLITLTSRSNAQROEISAFAKTLFGRLDLDKSE 72

Search completed: April 8, 2004, 11:56:50
Job time : 56 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:50:30 ; Search time 20 Seconds
(without alignments)
230.860 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72
Perfect score: 231
Sequence: 1 RKMKGIGDEESILFTLTS.....ISAFKTLFGRIIDLDKSE 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	231	100.0	320 1 AOHUP	annexin V [validat
2	224	97.0	320 1 S27214	annexin V - bovine
3	206	89.2	321 1 LUCB5	annexin V - chick
4	194	84.0	319 1 LURF5	annexin V - rat
5	173	74.9	319 1 LUBO4	annexin IV - bovin
6	172	74.5	318 1 LUPG4	annexin IV - pig
7	169	73.2	463 2 S29170	annexin VII - mus
8	167	72.3	321 1 A42077	annexin IV - human
9	167	72.3	673 1 AOHU68	annexin VI [valida
10	166	71.9	157 2 S09020	annexin VI [chicken
11	166	71.9	671 2 JC2029	annexin VI - mouse
12	164	71.0	673 1 S01786	annexin VII, long
13	163	70.6	488 1 LURH7	annexin VI - rat
14	162	70.1	673 1 S52844	annexin XI, form A
15	159	68.8	503 1 LUBO11	annexin XI - rabbi
16	159	68.8	503 1 LURB11	annexin XI form B
17	159	68.8	505 1 S23447	annexin XI - human
18	159	68.8	505 2 A53152	annexin XI - human
19	156	67.5	316 1 LUCF12	annexin XII - Hydr
20	150	64.9	327 1 LURH8	annexin VIII - hum
21	149.5	64.7	512 2 S70644	annexin VII - Afri
22	148	64.1	296 2 LURF9	annexin IX - fruit
23	142	61.5	676 2 S41022	hypothetical prote
24	141	61.0	321 1 LURF10	annexin X - fruit
25	131	56.7	323 1 LURH3	annexin III - huma
26	124	53.7	324 1 LURF3	annexin III - rat
27	120	51.9	462 1 LUD07	annexin VII - slim
28	119	51.5	346 1 LURF1	annexin I - rat
29	118	51.1	346 1 LUMS1	annexin I - mouse

30	115	49.8	316 2 A57076	annexin XIIa -
31	115	49.8	321 2 A84809	probable annexi
32	115	49.8	357 2 B57076	annexin XIIb -
33	112	48.5	339 1 LUBO36	annexin II - bo
34	112	48.5	343 1 A44118	annexin I type
35	111	48.1	339 1 LURH36	annexin II - hu
36	111	48.1	339 1 LUMS36	annexin II - mo
37	111	48.1	339 2 S33700	annexin II - rat
38	111	48.1	341 2 S55277	annexin II - ra
39	110	47.6	346 1 LURH1	annexin XII, g
40	109	47.2	316 1 LURH5	annexin I - hum
41	108	46.8	346 1 LURH	annexin, isofo
42	104	45.0	315 2 T06322	annexin I - ch
43	102	44.2	130 2 S36103	annexin I - bo
44	102	44.2	346 1 S28228	annexin I typ
45	100	43.3	340 1 JQ1298	annexin II typ

ALIGNMENTS

RESULT 1

AOHUP

annexin V [validated] - human

N/Alternate names: endonexin II; lipocortin V; placental anticoagulant pr

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-20

C/Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C319

R/Peptidase: R. B.; Tizard, R.; Mattaliano, R.C.; Sinclair, L.K.; Miller, G

U/Biol. Chem. 263, 10799-10811, 1988

A/Title: Five distinct calcium and phospholipid binding proteins share ho

A/Reference number: A92659; MUID:88273202; PMID:2968983

A/Accession: D29250

A/Molecule type: mRNA

A/Residues: 1-320 <PEP>

A/Cross-references: GB:M21731; NID:G186969; PIDN:AA36166.1; PID:G307116

R/Gundmann, U.; Abel, K.J.; Bohm, H.; Loebmann, H.; Lottspeich, F.; Ku

Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988

A/Title: Characterization of cDNA encoding human placental anticoagulant

A/Reference number: A30206; MUID:88234495; PMID:2967495

A/Accession: A30206

A/Molecule type: mRNA

A/Residues: 1-320 <GRU>

A/Cross-references: GB:M19384; NID:G189614; PIDN:AA59545.1; PID:G189615

R/Kaplan, R.; Jave, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.

J. Biol. Chem. 263, 8037-8043, 1988

A/Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+)

A/Reference number: A28076; MUID:88228020; PMID:2967291

A/Accession: A28076

A/Molecule type: mRNA

A/Residues: 1-320 <KAP>

A/Cross-references: GB:J03745; NID:G182111; PIDN:AA52366.1; PID:G182112

R/Maurer-Pog, I.; Reuteling-Sperger, C.P.M.; Plesters, J.; Bodo, G.; Sira

Eur. J. Biochem. 174, 585-592, 1988

A/Title: Cloning and expression of cDNA for human vascular anticoagulant

A/Reference number: S01016; MUID:88271329; PMID:2455636

A/Accession: S01016

A/Molecule type: mRNA

A/Residues: 1-320 <AMU>

A/Cross-references: EMBL:X12454; NID:G37636; PIDN:CAA30955.1; PID:G37637

A/Note: part of this sequence was confirmed by protein sequencing

R/Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.

Biochemistry 26, 8087-8092, 1987

A/Title: Primary structure of human placental anticoagulant protein.

A/Reference number: A29417; MUID:88163463; PMID:2964863

A/Accession: A29417

A/Molecule type: mRNA

A/Residues: 1-320 <FUN>

A/Cross-references: EMBL:M18366; NID:G179131; PIDN:AA35570.1; PID:G1791

R/Iwasaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saito, Y.; Arai, K.; Mura

J. Biochem. 102, 1261-1273, 1987

A/Title: Structure and expression of cDNA for an inhibitor of blood coag

A:Reference number: A41514; MUID:88139278; PMID:2363810
A:Accession: A41514
A:Molecule type: mRNA
A:Residues: 1-320 <IWA>
A:Cross-References: GB:D00172; NID:9219480; PIDN:BA00122.1; PID:8219481
A:Note: part of this sequence was confirmed by protein sequencing
R:Schlaepfer, D.D.; Mehlmann, T.; Burgess, W.H.; Haigler, H.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987
A:Title: Structural and functional characterization of endonexin II, a calcium- and phospholipid-binding protein
A:Accession: A28038
A:Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
R:Ahm, N.G.; Teller, D.C.; Blenkowski, M.T.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase-A-2 inhibitor.
A:Reference number: A92696; MUID:89066652; PMID:2974032
A:Accession: C31953
A:Molecule type: protein
A:Residues: 85-93 <AHN>
R:Rochut, B.; Comer, C.; Cortal, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; C. Biochem. J. 263, 929-935, 1989
A:Title: A 32 kDa lipocortin from human mononuclear cells appears to be identical with the reference number: 506646; MUID:9008443; PMID:2532007
A:Accession: S06646
A:Molecule type: protein
A:Residues: 7-25, 27-42, 51-74, 'X', 76-151, 181-198, 202-207, 209-226, 228-238, 246-271, 277-282; FEBS Lett. 275, 15-21, 1990
R:Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.
A:Title: The calcium binding sites in human annexin V by crystal structure analysis at 2 A:Reference number: A37250; MUID:91085549; PMID:218156
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
R:Funakoshi, T.; Helmark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
Biochemistry 26, 5572-5578, 1987
A:Title: Human placental anticoagulant protein: isolation and characterization.
A:Reference number: A29670; MUID:88050845; PMID:2960376
A:Accession: A29670
A:Molecule type: protein
A:Residues: 29-73, 274-297, 300-320 <FU2>
R:Fernandez, M.P.; Morgan, R.O.; Fernandez, M.R.; Careedo, M.T.
Gene 149, 253-260, 1994
A:Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C content
A:Reference number: I37172; MUID:95047484; PMID:7958998
A:Accession: I37172
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-320 <RES>
A:Cross-References: EMBL:U01691; NID:9430964; PIDN:AA04047.1; PID:9430966
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid bilipid-binding rather than proteolytic inactivation. It does not affect thrombin-dependent clotting.
C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation
C:Genetics:
A:Gene: GDB:ANX5
A:Cross-References: GDB:120555; OMIM:131230
A:Map position: 4Q26-4Q28
A:Introns: 3/3, 32/1, 63/3, 101/3, 132/1, 158/3, 177/3, 209/1, 241/1, 260/3, 301/3
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin F;12-320/Produce: annexin V #status experimental <MAT>
F:18-89/Domain: annexin repeat homology <AX1>
F:29-45/Region: endonexin fold #status predicted
F:90-161/Domain: endonexin repeat homology <AX2>
F:173-245/Region: endonexin repeat homology <AX3>
F:173-245/Domain: endonexin repeat homology <AX2>
F:185-201/Region: endonexin fold #status predicted
F:249-320/Domain: annexin repeat homology <AX4>
F:260-276/Region: endonexin repeat homology <AX4>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:2/Binding site: phosphorylated (Thr) (covalent) #status predicted
F:28,30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experimental

F:33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental
F:73,78/Binding site: calcium, low affinity (Ileu, Glu) #status experimental
F:100,102,104,144/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status experimental
F:259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status experimental
Query Match 100.0%; Score 231, DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDLKSE 48
DB 25 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDLKSE 72
RESULT 2
S27214
annexin V - bovine
N:Alternate names: CABP33, CABP37
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C:Accession: S27214; S27215
R:Leamonth, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Giambanco, I.; B. Biochim. Biophys. Acta 1160, 76-83, 1992
A:Title: Novel isoforms of CABP 33/37 (Annexin V) from mammalian brain: structural and p
A:Reference number: S27214; MUID:93041974; PMID:1420335
A:Accession: S27214
A:Molecule type: protein
A:Residues: 1-320 <LEA>
A:Accession: S27215
A:Molecule type: protein
A:Residues: 1-35, 'T', 37-124, 'E', 126-320 <LE2>
A:Note: It is uncertain whether the sequence differences are due to allelic variation or
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid bilipid-binding rather than proteolytic inactivation. It does not affect thrombin-dependent clotting.
C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin F:17-88/Domain: endonexin repeat homology <AX1>
F:28-44/Region: endonexin fold #status predicted
F:89-160/Domain: endonexin repeat homology <AX2>
F:100-116/Region: endonexin repeat homology <AX2>
F:172-244/Domain: annexin repeat homology <AX3>
F:184-200/Region: endonexin fold #status predicted
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin fold #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:2/Binding site: phosphorylated (Thr) (covalent) #status experimental
F:7,29,31,71/Binding site: calcium, high affinity (Met, Gly, Glu, Glu) #status predicted
F:32,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F:72,77/Binding site: calcium, low affinity (Ileu, Glu) #status predicted
F:99,101,103,143/Binding site: calcium, high affinity (Ileu, Gly, Gly, Asp) #status predicted
F:258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
Query Match 97.0%; Score 224, DB 1; Length 320;
Best Local Similarity 95.8%; Pred. No. 2.4e-20;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDLKSE 48
DB 24 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDLKSE 71
RESULT 3
LUCBS
annexin V - chicken
N:Alternate names: anchorin CIT; endonexin II; lipocortin V; placental anticoagulant protein
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000
C:Accession: A35381; A28623; B40404; S32523; S08771
R:Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfeafle, M.; Deutzmann, R.; M. J. Biol. Chem. 265, 8344, 1990
A:Reference number: A35381; MUID:90243721; PMID:2159478

A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-44;72-77;112-119;163-180;181-190;226-235 <SOH>
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid dectocod.
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin
F:12-319/Product: annexin IV #status predicted <MAY>
F:17-88/Domain: annexin repeat homology <AX1>
F:28-44/Region: endonexin fold #status predicted
F:89-160/Domain: annexin repeat homology <AX2>
F:100-116/Region: endonexin fold #status predicted
F:172-244/Domain: annexin repeat homology <AX3>
F:184-200/Region: endonexin fold #status predicted
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin fold #status predicted
F:7/Binding site: phosphate (Thr) (covalent) #status predicted
F:125,245/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 74.9%; Score 173; DB 1; Length 319;
Best Local Similarity 70.8%; Pred. No. 5.7e-14;
Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

RESULT 6
LURC4
annexin IV - pig
N:Alternate names: 32k calelectrin; chrymbindin IV; endonexin; lipocortin IV; protein I
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 24-Nov-1999
C:Accession: A27107
R:Weber, K.; Johnson, N.; Plesmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; Vandekeckht
EMBO J. 6, 1599-1604, 1987
A:Title: The amino acid sequence of protein II and its phosphorylation site for protein
A:Reference number: A27107; MUID:87275850; PMID:2956093
A:Accession: A27107
A:Molecule type: protein
A:Residues: 1-318 <MEB>
A:Experimental source: intestinal epithelium
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid dectocod.

C:Superfamily: annexin I; annexin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprotein
F:16-87/Domain: annexin repeat homology <AX1>
F:27-43/Region: endonexin fold #status predicted
F:88-159/Domain: annexin repeat homology <AX2>
F:171-243/Domain: annexin repeat homology <AX3>
F:183-199/Region: endonexin fold #status predicted
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: endonexin fold #status predicted
F:6/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:124,244/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 74.5%; Score 172; DB 1; Length 318;
Best Local Similarity 70.8%; Pred. No. 7.6e-14;
Matches 34; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 RKAMKGLCTDEBSITLTLTSRSMNQRQETSAFRTLFGRLDLDLKKSE 48
Db 23 RKAMKGLCTDEBSITLTLTSRSMNQRQETSAFRTLFGRLDLDLKKSE 70

RESULT 7
S29170
annexin VII - mouse
N:Alternate names: synexin
C:Species: Mus musculus (house mouse)

C:Date: 25-Feb-1994 #sequence revision 01-Sep-1995 #text_change 13-Aug-1999
C:Accession: S29170; S46209; S51173
R:Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.
Biochem. J. 289, 735-741, 1993
A:Title: Mouse synexin (annexin VII) polymorphisms and a phylogenetic comparison with oct
A:Reference number: S29170; MUID:93168121; PMID:7916616
A:Accession: S29170
A:Molecule type: mRNA
A:Residues: 1-463 <ZHA>
A:Cross-references: EMBL:L13129
R:Zhang-Keck, Z.Y.; Srivastava, M.; Kozak, C.A.; Chohuy, H.; Shirvan, A.; Burns, A.L.; R
Biochem. J. 301, 835-845, 1994
A:Title: Genomic organization and chromosomal localization of the mouse synexin gene.
A:Reference number: S46209; MUID:94330961; PMID:8053905
A:Accession: S46209
A:Molecule type: DNA
A:Residues: 1-463 <ZHF>
R:Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.
submitted to the EMBL Data Library, May 1993
A:Reference number: S51173
A:Accession: S51173
A:Molecule type: mRNA
A:Residues: 1-144, 'S', 146-303, 'A', 305-463 <ZHW>
A:Cross-references: EMBL:L13129; NID:9293293; PIDN:AAA37238.1; PID:9293294
A:Gene: MGI:Anx7
A:Cross-references: MGI:88031
A:Map position: 14
A:Insertions: 19/3; 87/1; 121/1; 142/3; 177/1; 208/3; 246/3; 303/3; 360/3; 386/1; 423/3
C:Superfamily: annexin VII; annexin repeat homology
C:Keywords: calcium channel; ion channel
F:163-234/Domain: annexin repeat homology <AX1>
F:235-306/Domain: annexin repeat homology <AX2>
F:318-390/Domain: annexin repeat homology <AX3>
F:394-463/Domain: annexin repeat homology <AX4>

Query Match 73.2%; Score 169; DB 2; Length 463;
Best Local Similarity 64.6%; Pred. No. 2.7e-13;
Matches 31; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 1 RKAMKGLCTDEBSITLTLTSRSMNQRQETSAFRTLFGRLDLDLKKSE 48
Db 170 RKAMKGLCTDEBSITLTLTSRSMNQRQETSAFRTLFGRLDLDLKKSE 217

RESULT 8
A42077
annexin IV - human
N:Alternate names: endonexin I; placental anticoagulant protein II; PP4-X protein
C:Species: Homo sapiens (man)
C:Date: 30-Jan-1993 #sequence revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: A42077; S07434; A31953; A31046
R:Rait, J.F.; Smith, C.; Frankberry, D.A.; Miao, C.H.; Adler, D.A.; Distche, C.M.
Genomics 12, 313-318, 1992
A:Title: Chromosomal mapping of the human annexin IV (ANX4) gene.
A:Reference number: A42077; MUID:92155721; PMID:1346776
A:Accession: A42077
A:Molecule type: mRNA
A:Residues: 1-321 <TAI>
A:Cross-references: CB:M82809; NID:9178698; PIDN:AAA51740.1; PID:9178699
A:Accession: B42077
A:Molecule type: DNA
A:Residues: 87-129 <TA2>
R:Grundmann, U.; Amann, E.; Abel, K.J.; Kuepper, H.A.
Behring Inst. Mitt. 82, 59-67, 1988
A:Title: Isolation and expression of cDNA coding for a new member of the phospholipase A.
A:Reference number: S07434; MUID:88309022; PMID:2970257
A:Accession: S07434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97, 'Q', 99-321 <GRU>
A:Cross-references: EMBL:M9383; NID:9189616; PIDN:AA041689.1; PID:9189617
R:Ahm, N.G.; Teller, D.C.; Blenkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.

J. Biol. Chem. 263, 18657-18663, 1988.
 A>Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2 isozymes.
 A:Reference number: A92696; PMID:8906652; PMID:2974032
 A:Accession: A31953
 A:Molecule type: protein
 A:Residues: 29-58;101-126;282-310 <A>
 R:Raitt, J.F.; Sakata, M.; McMullen, B.A.; Mao, C.H.; Funakoshi, T.; Hendrickson, L.E.; Biochemistry 27, 6268-6276, 1988
 A>Title: Placental anticoagulant proteins: isolation and comparative characterization of A, B, and C isoforms.
 A:Reference number: A90534; PMID:89118212; PMID:2975506
 A:Accession: A31046
 A:Molecule type: protein
 A:Residues: 4-17;30-74;102-146;283-321 <A>
 C:Genetics:
 A:Gene: GDB:ANX4
 A:Cross-references: GDB:131395; OMIM:106491
 A:Map position: 2p13-2p13
 A:Introns: 102/3
 C:Superfamily: annexin I; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; glycoprotein
 F:2-321/Product: annexin IV #status predicted <A>
 F:19-90/Domain: annexin repeat homology <AX1>
 F:30-46/Region: endonexin fold #status predicted
 F:91-162/Domain: annexin repeat homology <AX2>
 F:102-118/Region: endonexin fold #status predicted
 F:174-246/Domain: annexin repeat homology <AX3>
 F:186-202/Region: endonexin fold #status predicted
 F:250-321/Domain: annexin repeat homology <AX4>
 F:261-277/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
 F:9/Binding site: phosphate (Thr) (covalent) #status predicted
 F:247/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.3%; Score 167; DB 1; Length 321;
 Best Local Similarity 66.7%; Pred. No. 3; 2e-13;
 Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESILTLTSRNSAQRQESIAFKTLFGRLDLDLXSE 48
 DB 26 RKAMKGLTDEDAITISVLAHYRNTAQRQELRTAYKSTIGRLDLDLXSE 73

RESULT 9
 AOHU68
 annexin VI [validated] - human
 N:Alternate names: calcium-binding protein, 68k, calelectrin, calphobindin II
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence revision 30-Sep-1992 #text change 08-Dec-2000
 C:Accession: J00032; S00263; S18519; A31079; B34459; B31953; A53507
 R:Yasuda, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Saito, Y.; Shiojima, T.; Biochem. 106, 43-49, 1989
 A>Title: Structure and expression of cDNA for calphobindin II, a human placental coagulant protein.
 A:Reference number: J00032; PMID:89380132; PMID:2528541
 A:Accession: J00032
 A:Molecule type: mRNA
 A:Residues: 1-673 <A>
 A:Cross-references: EMBL:D00510; NID:9219550; PDB:BA00400.1; PDB:9219551
 R:Crumpson, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crumpson, M.J.; EMBO J. 7, 21-27, 1988
 A>Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p68.
 A:Reference number: S00263; PMID:89196081; PMID:3258820
 A:Accession: S00263
 A:Molecule type: mRNA
 A:Residues: 1-618; 'D', 620-673 <CR1>
 A:Cross-references: EMBL:Y00097; NID:935217; PDB:CAA68286.1; PDB:935218
 A:Accession: S18519
 A:Molecule type: protein
 A:Residues: 103-113;167-172, 'X', 174-177;232-235, 'F', 237-240;251-258;277-281;359-362, 'G', 'A';Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-Glu
 A>Note: eight calcium ions are bound in the presence of phospholipid
 R:Stuehn, T.C.; Slaughter, C.A.; Leznicki, I.; Barton, P.; Reynolds, G.A. Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988

A>Title: Human 67-kDa calelectrin contains a duplication of four repeats of the annexin repeat.
 A:Reference number: A31079; PMID:88124902; PMID:2963335
 A:Accession: A31079
 A:Molecule type: mRNA
 A:Residues: 1-225; 'NK', 228-554, 'T', 556-673 <SUE>
 A:Cross-references: GB:J03578; NID:9179975; PDB:AAA5656.1; PDB:9179976
 R:Yoshizaki, H.; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Shidara, Y.; Maeda, T.; Biochem. 107, 43-50, 1990
 A>Title: Structure and properties of calphobindin II, an anticoagulant protein.
 A:Reference number: J00091; PMID:90236978; PMID:2139657
 A:Accession: J00091
 A:Molecule type: protein
 A:Residues: 2-299;307-314;320-445;447-549;581-673 <Y08>
 R:Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T. J. Biol. Chem. 264, 17222-17230, 1989
 A>Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-A:Reference number: A34459; PMID:90008880; PMID:2529258
 A:Accession: B34459
 A:Molecule type: protein
 A:Residues: 10-25;69-75;136-151;192-207;209-220;300-306 <HAY>
 A:Experimental source: Placenta
 R:Rahm, N.G.; Jeller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W. J. Biol. Chem. 263, 18657-18663, 1988
 A>Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2 isozymes.
 A:Reference number: A92696; PMID:8906652; PMID:2974032
 A:Accession: B31953
 A:Molecule type: protein
 A:Residues: 90-108; 'L', 110-126;127, 265-276;286-302;626-654 <A>
 R:Hyatt, S.L.; Liao, L.; Chapline, C.; Jaken, S. Biochemistry 33, 1223-1228, 1994
 A>Title: Identification and characterization of alpha-protein kinase C beta 1 and beta 2 isoforms.
 A:Reference number: A53507; PMID:94153907; PMID:810754
 A:Accession: A53507
 A:Molecule type: protein
 A:Residues: 'X', 473-480, 'DY', <HYA>
 C:Comment: This abundant cytosolic protein binds to the inner surface of the plasma membrane.
 C:Genetics:
 A:Gene: GDB:ANX6
 A:Cross-references: GDB:119681; OMIM:114070
 A:Map position: 5q32-5q34
 C:Superfamily: annexin VI; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold
 F:2-673/Product: annexin VI #status experimental <A>
 F:23-94/Domain: endonexin repeat homology <AX1>
 F:34-50/Region: endonexin fold #status predicted
 F:95-166/Domain: annexin repeat homology <AX2>
 F:106-122/Region: endonexin fold #status predicted
 F:178-250/Domain: annexin repeat homology <AX3>
 F:190-206/Region: endonexin fold #status predicted
 F:224-325/Domain: annexin repeat homology <AX4>
 F:265-281/Region: endonexin fold #status predicted
 F:366-437/Domain: annexin repeat homology <AX5>
 F:377-393/Region: endonexin fold #status predicted
 F:438-509/Domain: annexin repeat homology <AX6>
 F:449-465/Region: endonexin fold #status predicted
 F:527-588/Domain: annexin repeat homology <AX7>
 F:538-554/Region: endonexin fold #status predicted
 F:602-673/Domain: annexin repeat homology <AX8>
 F:613-629/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 72.3%; Score 167; DB 1; Length 673;
 Best Local Similarity 66.7%; Pred. No. 7; 4e-11;
 Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESILTLTSRNSAQRQESIAFKTLFGRLDLDLXSE 48
 DB 373 RKAMKGLTDEDTIIDITHSNVQRQELRTAYKSTIGRLDLDLXSE 420

RESULT 10
 S09020

calcimedin, 32K - chicken (fragments)
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Nov-1993 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
 C/Accession: S09020
 R/Kobayashi, R.; Hidaka, H.; Tashima, Y.
 Arch. Biochem. Biophys. 277, 203-210, 1990
 A/Title: Purification, characterization, and partial sequence analysis of 32-kDa calcime
 A/Reference number: S09020; MUID:90165469; PMID:2137684
 A/Accession: S09020
 A/Molecule type: protein
 A/Residues: 1-36;37-53;54-64;65-81;82-105;106-116;117-137;138-150;151-157 <KOB>
 C/Comment: Annexin undergo reversible, calcium-dependent binding to membrane phospholip
 deroosd.

C/Superfamily: annexin I; annexin repeat homology
 C/Keywords: blocked amino end; calcium binding; collagen binding; duplication; endonexin
 F/15-36/Domain: annexin repeat homology (Fragment) <AX1A>
 F/37-53/Domain: annexin repeat homology (Fragment) <AX1B>
 F/54-64/Domain: annexin repeat homology (Fragment) <AX1C>
 F/65-71/Domain: annexin repeat homology (Fragment) <AX1D>
 F/72-102/Domain: annexin repeat homology (Fragment) <AX2A>
 F/103-116/Domain: annexin repeat homology (Fragment) <AX2B>
 F/117-137/Domain: annexin repeat homology (Fragment) <AX3A>
 F/138-150/Domain: annexin repeat homology (Fragment) <AX3B>
 F/30,32,33/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted

Query Match 71.9%; Score 166; DB 2; Length 157;
 Best Local Similarity 80.0%; Pred. No. 1.9e-13;
 Matches 36; Conservative 6; Mismatches 1; Indels 2; Gaps 2;

OY 1 RKAMKGLTDEESITLTLTSSNAQROEISAAFTLFGDLDDLDL 45
 Db 22 RKAMKGLTDEESITLTLTSSNAQROEISAAFTLFGDLDDLDL 64

RESULT 11
 JC2029
 N/Alternate names: annexin - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
 C/Accession: JC2029
 R/Cao, X.; Genge, B.R.; Wu, L.N.Y.; Buzzzi, W.R.; Showman, R.M.; Wuthier, R.E.
 Biochem. Biophys. Res. Commun. 197, 556-561, 1993
 A/Title: Characterization, cloning and expression of the 67-kDa annexin from chicken gro
 A/Reference number: JC2029; MUID:94092130; PMID:8267550
 A/Accession: JC2029
 A/Molecule type: mRNA
 A/Residues: 1-671 <CAO>
 C/Superfamily: annexin VI; annexin repeat homology
 C/Keywords: calcium binding; phospholipid binding
 F/21-92/Domain: annexin repeat homology <AX1>
 F/93-164/Domain: annexin repeat homology <AX2>
 F/176-248/Domain: annexin repeat homology <AX3>
 F/252-323/Domain: annexin repeat homology <AX4>
 F/364-435/Domain: annexin repeat homology <AX5>
 F/436-507/Domain: annexin repeat homology <AX6>
 F/525-597/Domain: annexin repeat homology <AX7>
 F/601-671/Domain: annexin repeat homology <AX8>

Query Match 71.9%; Score 166; DB 2; Length 671;
 Best Local Similarity 70.8%; Pred. No. 9.8e-13;
 Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 RKAMKGLTDEESITLTLTSSNAQROEISAAFTLFGDLDDLDL 48
 Db 371 RKAMKGLTDEESITLTLTSSNAQROEISAAFTLFGDLDDLDL 418

RESULT 12
 S01786
 N/Alternate names: calcium-binding protein p68; calelectrin; calphobindin II
 C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C/Accession: S01786
 R/Moss, S.E.; Crompton, M.R.; Crompton, M.J.
 Eur. J. Biochem. 177, 21-27, 1989
 A/Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family
 A/Reference number: S01786; MUID:89030687; PMID:2972541
 A/Accession: S01786
 A/Molecule type: mRNA
 A/Residues: 1-673 <MOS>

A/Cross-references: EMBL:X13460; NID:G53580; PIDN:CAA31808.1; PID:G53581
 A/Note: the authors translated the codon GCC for residue 329 as Gly
 C/Comment: This abundant cytosolic protein binds to the inner surface of the cell membrar
 C/Superfamily: annexin VI; annexin repeat homology
 C/Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosphol
 F/23-94/Domain: annexin repeat homology <AX1>
 F/34-50/Region: endonexin fold #status predicted
 F/95-166/Domain: annexin repeat homology <AX2>
 F/106-122/Region: endonexin fold #status predicted
 F/178-250/Domain: annexin repeat homology <AX3>
 F/190-206/Region: endonexin fold #status predicted
 F/254-325/Domain: annexin repeat homology <AX4>
 F/326-437/Region: endonexin fold #status predicted
 F/366-437/Domain: annexin repeat homology <AX5>
 F/377-393/Region: endonexin fold #status predicted
 F/438-509/Domain: annexin repeat homology <AX6>
 F/449-465/Region: endonexin repeat homology <AX6>
 F/527-598/Domain: annexin repeat homology <AX7>
 F/538-554/Region: endonexin fold #status predicted
 F/602-673/Domain: annexin repeat homology <AX8>
 F/613-629/Region: endonexin fold #status predicted
 F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 71.0%; Score 164; DB 1; Length 673;
 Best Local Similarity 66.7%; Pred. No. 1.7e-12;
 Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 1 RKAMKGLTDEESITLTLTSSNAQROEISAAFTLFGDLDDLDL 48
 Db 373 RKAMKGLTDEESITLTLTSSNAQROEISAAFTLFGDLDDLDL 420

RESULT 13
 L0H07
 N/Alternate names: annexin VII, long form - human
 N/Contains: annexin VII, long form; annexin VII, short form
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1992 #sequence_revision 26-Jan-1996 #text_change 22-Jun-1999
 C/Accession: A54467; A32554; A39513; B39513
 R/Shivan, A.; Srivastava, M.; Wang, M.G.; Cultraro, C.; Magendzo, K.; McBride, O.W.; Pol
 Biochemistry 33, 6888-6901, 1994
 A/Title: Divergent structure of the human synexin (annexin VII) gene and assignment to cl
 A/Reference number: A54467; MUID:94264005; PMID:7515686
 A/Accession: A54467
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-488 <SHI>
 R/Burns, A.L.; Magendzo, K.; Shivan, A.; Srivastava, M.; Rojas, E.; Alljani, M.R.; Polle
 Proc. Natl. Acad. Sci. U.S.A. 86, 3796-3802, 1989
 A/Title: Calcium channel activity of purified human synexin and structure of the human sy
 A/Reference number: A32554; MUID:89264510; PMID:2542947
 A/Accession: A32554
 A/Molecule type: mRNA
 A/Residues: 1-145;168-488 <BUR>

A/Cross-references: EMBL:J04543; NID:G338243; PIDN:AAA36616.1; PID:G338244
 R/Magendzo, K.; Shivan, A.; Cultraro, C.; Srivastava, M.; Pollard, H.B.; Burns, A.L.
 J. Biol. Chem. 266, 3228-3232, 1991
 A/Title: Alternative splicing of human synexin mRNA in brain, cardiac, and skeletal muscl
 A/Reference number: A39513; MUID:91131630; PMID:1825209
 A/Accession: A39513
 A/Molecule type: mRNA
 A/Residues: 137-145;168-176 <MAG>

A/Cross-references: EMBL:J05732
A/Accession: B39513
A/Molecule type: mRNA
A/Residues: 137-176 <MA2>
C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid.
C/Comment: The long form of annexin VII is more prevalent in brain, heart, and skeletal muscle.
C/Genetics:
A/Gene: GDB:ANX7
A/Cross-references: GDB:369042; OMIM:186360
A/Map position: 10q21.1-10q21.2
A/Introns: 17/3; 87/1; 124/1; 145/3; 167/3; 202/2; 233/3; 271/3; 328/3; 385/3; 411/1; 44
C/Superfamily: annexin VII; annexin repeat homology
C/Keywords: alternative splicing; calcium binding; calcium channel; duplication; endonex
F/1-145/488/Product: annexin VII, long form #status predicted <MA2>
F/1-145/168-488/Product: annexin VII, short form #status predicted <MA3>
F/188-259/Domain: annexin repeat homology <AX1>
F/189-215/Region: endonexin fold #status predicted
F/260-331/Domain: annexin repeat homology <AX2>
F/271-287/Region: endonexin fold #status predicted
F/343-415/Domain: annexin repeat homology <AX3>
F/355-371/Region: endonexin fold #status predicted
F/419-488/Domain: annexin repeat homology <AX4>
F/430-446/Region: endonexin fold #status predicted

Query Match 70.6%; Score 163; DB 1; Length 488;
Best Local Similarity 64.6%; Pred. No. 1.6e-12;
Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFFKTLFGRLDLDLXSE 48
Db 195 RKAMKGTDEQALIVDVANRSNDQROKIKAAFTSYKDLIXDKSE 242

RESULT 14
S52844
annexin VI - rat
N/Alternate names: calcium-binding protein 65/67
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S65683; S52844
C/Author: H. J. Josic, D. J. Lim, Y. P. Reuter, W.
Burr, J. Biochem 230, 741-751, 1995
A/Title: CDNA cloning and tissue-specific regulation of expression of rat calcium-binding
A/Reference number: S65683; MIM:9531313; PMID:7607247
A/Accession: S65683
A/Molecule type: mRNA
A/Residues: 1-673 <FAN>
A/Cross-references: EMBL:X86086; NID:g763180; PIDD:CA60040.1; PIDD:g763181
A/Experimental source: liver
C/Superfamily: annexin VI; annexin repeat homology
C/Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associated
F/2-673/Product: annexin VI #status predicted <MA2>
F/23-94/Domain: annexin repeat homology <AX1>
F/34-50/Region: endonexin fold #status predicted
F/59-166/Domain: annexin repeat homology <AX2>
F/106-122/Region: endonexin fold #status predicted
F/178-250/Domain: annexin repeat homology <AX3>
F/180-206/Region: endonexin fold #status predicted
F/254-325/Domain: annexin repeat homology <AX4>
F/265-281/Region: endonexin fold #status predicted
F/366-437/Domain: annexin repeat homology <AX5>
F/377-393/Region: endonexin fold #status predicted
F/438-509/Domain: annexin repeat homology <AX6>
F/449-465/Region: endonexin fold #status predicted
F/527-598/Domain: annexin repeat homology <AX7>
F/538-554/Region: endonexin fold #status predicted
F/602-673/Domain: annexin repeat homology <AX8>
F/613-629/Region: endonexin fold #status predicted
F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 70.1%; Score 162; DB 1; Length 673;
Best Local Similarity 64.6%; Pred. No. 3.1e-12;

Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFFKTLFGRLDLDLXSE 48
Db 373 RKAMKGTDEATITDITGRNVQRQIRQRFKSHFGRLDLDLXSE 420

RESULT 15
LUBO11
annexin XI form A - bovine
N/Alternate names: calyculin-associated protein peptide, CAP-50
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C/Accession: A42113; A42909; B42909; C42909; D42909
R/Towle, C.A.; Treadwell, B.V.
J. Biol. Chem. 267, 5416-5423, 1992
A/Title: Identification of a novel mammalian annexin. cDNA cloning, sequen
A/Reference number: A42113; MIM:92184796; PMID:1372001
A/Accession: A42113
A/Molecule type: mRNA
A/Residues: 1-503 <TOW>
A/Cross-references: GB:M82802; NID:g162673; PIDD:AAA0379.1; PIDD:g162674
A/Note: the authors did not translate the codon GAC for residue 503
R/Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi
J. Biol. Chem. 267, 13498-13504, 1992
A/Title: CAP-50, a newly identified annexin, localizes in nuclei of cultur
A/Reference number: A42909; MIM:92317074; PMID:1618651
A/Accession: A42909
A/Molecule type: protein
A/Residues: 213-223 'X', 225-226/319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-33
A/Experimental source: lung
A/Note: sequence modified after extraction from NCBI backbone
C/Comment: Annexins undergo reversible, calcium-dependent binding to membr
derstood.
C/Genetics:
A/Introns: 19/1; 56/2
A/Note: the list of introns is incomplete
C/Superfamily: annexin VII; annexin repeat homology
C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; p
F/201-272/Domain: annexin repeat homology <AX1>
F/212-228/Region: endonexin fold #status predicted
F/273-344/Domain: annexin repeat homology <AX2>
F/284-300/Region: endonexin fold #status predicted
F/356-428/Domain: annexin repeat homology <AX3>
F/368-384/Region: endonexin fold #status predicted
F/432-503/Domain: annexin repeat homology <AX4>
F/443-459/Region: endonexin fold #status predicted
F/59/111/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.8%; Score 159; DB 1; Length 503;
Best Local Similarity 64.6%; Pred. No. 5.3e-12;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFFKTLFGRLDLDLXSE 48
Db 208 RKAMKGTDEQALIDCGSRNKQRQILSLFTAVGKDLIXDKSE 255

Search completed: Apr 11 8, 2004, 11:58:39
Job time : 21 sec

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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:55:51 ; Search time 23 Seconds

(without alignments)
107,741 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72

Perfect score: 231
Sequence: 1 RKAAGLGLDEESILFLTS.....ISNAFKTLGRDLDDKSE 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/6CTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	231	100.0	319	1	US-08-125-746-1 Sequence 1, Appli
2	231	100.0	320	1	US-08-125-746-3 Sequence 3, Appli
3	231	100.0	320	4	US-08-948-276-1 Sequence 1, Appli
4	231	100.0	320	6	5225537-4 Patent No. 5225537
5	231	100.0	327	4	US-09-324-096A-2 Sequence 2, Appli
6	231	100.0	327	4	US-09-324-096A-4 Sequence 6, Appli
7	231	100.0	327	4	US-09-324-096A-6 Sequence 2, Appli
8	207	89.6	319	4	US-08-948-276-2 Sequence 3, Appli
9	194	84.0	318	4	US-08-948-276-3 Sequence 2, Appli
10	194	84.0	319	2	US-08-149-975A-2 Sequence 14, Appli
11	173	74.9	319	3	US-08-526-136-14 Sequence 4, Appli
12	167	72.3	321	4	US-08-948-276-4 Sequence 13, Appli
13	163	70.6	466	3	US-08-526-136-13 Sequence 2, Appli
14	159	68.8	503	3	US-08-526-136-2 Sequence 4, Appli
15	159	68.8	505	3	US-08-526-136-4 Sequence 5, Appli
16	131	56.7	323	4	US-09-010-147B-16 Sequence 16, Appli
17	110	47.6	324	4	US-08-948-276-5 Sequence 6, Appli
18	108	46.8	346	4	US-09-919-172-39 Sequence 39, Appli
19	98	42.4	184	4	US-09-325-832A-65 Sequence 65, Appli
20	98	42.4	239	4	US-09-325-832A-65 Sequence 62, Appli
21	88	38.1	316	4	US-09-325-932A-62 Sequence 747, App
22	82	35.5	234	4	US-09-732-210-747 Sequence 220, App
23	63.5	27.5	93	4	US-09-634-238-220 Sequence 2, Appli
24	55.5	24.0	234	4	US-08-736-915-2 Sequence 24, Appli
25	54.5	23.6	335	3	US-08-091-219-24 Sequence 24, Appli
26	54.5	23.6	2318	4	US-09-660-541-24 Sequence 24, Appli
27	54.5	23.6	2318	4	US-09-660-541-24 Sequence 24, Appli

28	53.5	23.2	297	4	US-09-543-681A-6240
29	53.5	23.2	450	4	US-09-489-039A-13998
30	53.5	23.2	608	4	US-08-843-572E-2
31	53	22.9	1996	2	US-08-804-227C-9
32	53	22.9	1996	2	US-08-804-198-3
33	53	22.9	4545	2	US-08-804-227C-14
34	53	22.9	4550	2	US-08-804-227C-8
35	53	22.9	4550	2	US-08-804-198-2
36	52.5	22.7	392	4	US-09-489-039A-9827
37	52	22.5	151	4	US-09-621-976-4980
38	52	22.5	410	4	US-09-594-506-34
39	52	22.5	433	4	US-09-489-039A-8953
40	52	22.5	1037	4	US-09-543-681A-7677
41	52	22.5	1398	4	US-09-543-681A-5641
42	52	22.5	3768	4	US-09-336-447A-76
43	51.5	22.3	342	4	US-09-107-532A-5664
44	51	22.1	675	4	US-09-591-095-8
45	51	22.1	819	4	US-09-328-352-5342

ALIGNMENTS

RESULT 1
Sequence 1, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08125746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Ohlon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein

Sequence 6240,
Sequence 13998
Sequence 2, Ap
Sequence 9, Ap
Sequence 3, Ap
Sequence 14, A
Sequence 8, Ap
Sequence 9827,
Sequence 4980,
Sequence 34, A
Sequence 7677,
Sequence 5641,
Sequence 76, A
Sequence 5664
Sequence 8, Ap
Sequence 5342

US-08-125-746-1

Query Match 100.0%; Score 231; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 48
DB 24 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 71

RESULT 2

US-08-125-746-3
Sequence 3, Application US/08125746
Patent No. 5591633

GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: IWASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125.746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987

ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-125-746-3

Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 48
DB 25 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 72

RESULT 3

US-08-948-276-1

Sequence 1, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.

TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1
LENGTH: 320
TYPE: PRT
ORGANISM: human
US-08-948-276-1

Query Match 100.0%; Score 231; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 48
DB 25 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 72

RESULT 4

522537-4

APPLICANT: POSTER, DONALD
TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/459,082
FILING DATE: 29-DEC-1989
SEQ ID NO:4
LENGTH: 320

522537-4

Query Match 100.0%; Score 231; DB 6; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 48
DB 25 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 72

RESULT 5

US-09-324-096A-2

Sequence 2, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan

TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOPW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0

SEQ ID NO 2
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-2

Query Match 100.0%; Score 231; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSNAQROEISAFAKTLFGDLDLDDKSE 48

Thu Apr 8 13:28:54 2004

us-09-787-923-2_copy_25_72.apr082004.ra1

Db 32 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 6
US-09-324-096A-4
Sequence 4, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOPW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-4

Query Match 100.0%; Score 231; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
32 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 7
US-09-324-096A-6
Sequence 6, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOPW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-6

Query Match 100.0%; Score 231; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
32 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 8
US-08-948-276-2
Sequence 2, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2

LENGTH: 319
TYPE: PRT
ORGANISM: mouse
US-08-948-276-2

Query Match 89.6%; Score 207; DB 4; Length 319;
Best Local Similarity 87.5%; Pred. No. 1.5e-22;
Matches 42; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
23 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 70

RESULT 9
US-08-948-276-3
Sequence 3, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 318
TYPE: PRT
ORGANISM: rat
US-08-948-276-3

Query Match 84.0%; Score 194; DB 4; Length 318;
Best Local Similarity 79.2%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
22 RKAMKGLGTDEESITLTLTSSNAQROEISAFAKTLFGRLDLDLXSE 69

RESULT 10
US-08-149-975A-2
Sequence 2, Application US/08149975A
Patent No. 5849600
GENERAL INFORMATION:
APPLICANT: Nixon, Ralph
APPLICANT: Honda, Toshiyuki
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,975A
FILING DATE: 11-NOV-1993
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04843/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-149-975A-2

Query Match 84.0%; Score 194; DB 2; Length 319;
Best Local Similarity 79.2%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 48
DB 23 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 70

RESULT 11
US-08-526-136-14

Sequence 14, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:

APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036

FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 319
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-526-136-14

Query Match 74.9%; Score 173; DB 3; Length 319;
Best Local Similarity 70.8%; Pred. No. 1.7e-17;
Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 48
DB 34 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 48

DB 24 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 71

RESULT 12
US-08-948-276-4

Sequence 4, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: USCF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 321
TYPE: PRT
ORGANISM: human
US-08-948-276-4

Query Match 72.3%; Score 167; DB 4; Length 321;
Best Local Similarity 66.7%; Pred. No. 1.3e-16;
Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 48
DB 26 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 73

RESULT 13
US-08-526-136-13

Sequence 13, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:

APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036

FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
TYPE: amino acid

Query Match 74.9%; Score 173; DB 3; Length 319;
Best Local Similarity 70.8%; Pred. No. 1.7e-17;
Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 48
DB 34 RKAMKGLTDESDITLTLTSRNASQROEISAFKTLFGRLDLDKSE 48

Thu Apr 8 13:28:54 2004

us-09-787-923-2_copy_25_72.apr082004.ra1

Page

STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-526-136-13

Query Match
Best Local Similarity 64.6%; Score 163; DB 3; Length 466;
Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 RRAMKGLTDEESILTLTSRSNAQROEISAAFKTLFGRLDDLKSE 48
DB 173 RRAMKGFGTDEQAIIVDVANRSNDQKIKAAFKTSYGKDLIKDLKSE 220

RESULT 14
US-08-526-136-2
Sequence 2, Application US/08526136
Patent No. 6107089

GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-2

Query Match
Best Local Similarity 68.8%; Score 159; DB 3; Length 503;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY 1 RRAMKGLTDEESILTLTSRSNAQROEISAAFKTLFGRLDDLKSE 48
DB 208 RRAMKGFGTDEQAIIDCLGSRSNKQROQILISFKTAYGKDLIKDLKSE 255

RESULT 15
US-08-526-136-4
Sequence 4, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:

APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-4

Query Match
Best Local Similarity 68.8%; Score 159; DB 3; Length 505;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY 1 RRAMKGLTDEESILTLTSRSNAQROEISAAFKTLFGRLDDLKSE 48
DB 210 RRAMKGFGTDEQAIIDCLGSRSNKQROQILISFKTAYGKDLIKDLKSE 257

Search completed: April 8, 2004, 11:59:14
Job time: 23 secs

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TITLE OF INVENTION: of delta-PKC
FILE REFERENCE: 58600-8208.US00
CURRENT APPLICATION NUMBER: US/10/007,761
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/262,060
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-761-72

Query Match 100.0%; Score 231; DB 13; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 25 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 3
US-10-424-232-1
Sequence 1, Application US/10424232.
Publication No. US20040022731A1
GENERAL INFORMATION:
APPLICANT: Bogdanov, Alexei
APPLICANT: Schellenberger, Eyk
APPLICANT: Petrovsky, Alexander
APPLICANT: Josephson, Lee
TITLE OF INVENTION: In vivo Imaging of Apoptosis
FILE REFERENCE: 00786-549001
CURRENT APPLICATION NUMBER: US/10/424,232
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/60376,052
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-424-232-1

Query Match 100.0%; Score 231; DB 16; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 25 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 4
US-09-970-969-2
Sequence 2, Application US/09970969
Patent No. US20020103341A1
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-2

Query Match 100.0%; Score 231; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 32 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 5
US-09-970-969-4
Sequence 4, Application US/09970969
Patent No. US20020103341A1
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-4

Query Match 100.0%; Score 231; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 32 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 6
US-09-970-969-6
Sequence 6, Application US/09970969
Patent No. US20020103341A1
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-6

Query Match 100.0%; Score 231; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 32 RKAMKGLGDEESILTLTSSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 7
US-10-080-370-3
Sequence 3, Application US/10080370
Publication No. US20030166532A1
GENERAL INFORMATION:
APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis

```

FILE REFERENCE: SURR. 90
CURRENT APPLICATION NUMBER: US/10/080,370
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/332,582
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-10-080-370-3

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Query Match      84.0%; Score 194; DB 14; Length 319;
Best Local Similarity 79.2%; Pred. No. 5,6e-19;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 RKAMKGLGTDDESIITLTTSRNSAQRQEIISAFTKLPGRDLDDIKSE 48
Db      23 RKAMKGLGTDDESIITLTTSRNSAQRQEIISAFTKLPGRDLDDIKSE 70

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RESULT 8
US-10-080-370-6
Sequence 6, Application US/10080370
Publication No. US20030166532A1
GENERAL INFORMATION:
APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
FILE REFERENCE: SURR. 90
CURRENT APPLICATION NUMBER: US/10/080,370
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/332,582
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 669
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
NAME/KEY: misc feature
LOCATION: (334)..(334)
OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (351)..(351)
OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (45)..(45)
OTHER INFORMATION: n = a, c, g, or t
NAME/KEY: misc feature
LOCATION: (1000)..(1002)
OTHER INFORMATION: n = a, c, g, or t
NAME/KEY: misc feature
LOCATION: (1051)..(1053)
OTHER INFORMATION: n = a, c, g, or t
US-10-080-370-6

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Query Match      84.0%; Score 194; DB 14; Length 669;
Best Local Similarity 79.2%; Pred. No. 1,4e-18;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 RKAMKGLGTDDESIITLTTSRNSAQRQEIISAFTKLPGRDLDDIKSE 48
Db      37 RKAMKGLGTDDESIITLTTSRNSAQRQEIISAFTKLPGRDLDDIKSE 84

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RESULT 9
US-10-097-340-10
Sequence 10, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNANARAPU
APPLICANT: Sebastian HOBRSCHE
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIRY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMADT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins for The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-10

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Query Match      72.3%; Score 167; DB 14; Length 321;
Best Local Similarity 66.7%; Pred. No. 3,8e-15;
Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 RKAMKGLGTDDESIITLTTSRNSAQRQEIISAFTKLPGRDLDDIKSE 48
Db      26 RKAMKGLGTDDESIITLTTSRNSAQRQEIISAFTKLPGRDLDDIKSE 73

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RESULT 10
US-09-925-301-1062
Sequence 1062, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10

```

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PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 1062
LENGTH: 324
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-301-1062

Query Match      72.3%; Score 167; DB 9; Length 324;
Best Local Similarity 66.7%; Pred. No. 3.8e-15;
Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RKAMKGLGTDESIITLTSRSGNAQROEISAFAKTLFGDLDDDKSE 48
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Db 29 RKAMKGLGTDEDAISVLAHYNTAQROEIRTAVKSTIGDLIDDKSE 76

RESULT 11
US-10-114-270-160
Sequence 160, Application US/10114270
Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malysankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patuturajan, Meera
APPLICANT: Liu, Zhaozhong
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Li, Li
APPLICANT: Vernet, Corine
APPLICANT: Zernusen, Bryan D.
APPLICANT: Gorman, Linda
APPLICANT: Shenoy, Suresh G.
APPLICANT: Pena, Carol E. A.
APPLICANT: Smithson, Glenda
APPLICANT: Burgess, Catherine E.
APPLICANT: Gerlach, Valerie
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shinkets, Richard A.
APPLICANT: Gangolli, Bha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Ji, Weizhen
APPLICANT: Anderson, David W.
APPLICANT: Liete, Mario W.
APPLICANT: Rastelli, Luca
APPLICANT: Edinger, Shlomai R.
APPLICANT: Stone, David J.
APPLICANT: Macdougall, John R.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/282,934
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
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NUMBER OF SEQ ID NOS: 470
SEQ ID NO 160
LENGTH: 675
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-270-160

Query Match      72.3%; Score 167; DB 12; Length 675;
Best Local Similarity 66.7%; Pred. No. 9.9e-15;
Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 RKAMKGLGTDESIITLTSRSGNAQROEISAFAKTLFGDLDDDKSE 48
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Db 381 RKAMKGLGTDEDTITDITTHRSNVQRQIRQTFKSHFGRDMLTDKSE 428

RESULT 12
US-09-925-300-1664
Sequence 1664, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 1664
LENGTH: 485
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-300-1664

Query Match      70.6%; Score 163; DB 9; Length 485;
Best Local Similarity 64.6%; Pred. No. 2.4e-14;
Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RKAMKGLGTDESIITLTSRSGNAQROEISAFAKTLFGDLDDDKSE 48
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Db 192 RKAMKGFTEQAIIVDVNRSNDOROKTKAFAKTSYGDLIDDKSE 239

RESULT 13
US-10-236-031B-18
Sequence 18, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gordon, Gavin J.
APPLICANT: Jensen, Roderick V.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B00801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR FILING DATE: 2002-08-30
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NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-10-236-031B-18

Query Match 64.9%; Score 150; DB 15; Length 327;
Best Local Similarity 59.6%; Pred. No. 1e-12;
Matches 28; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KAMKGLTDEESITLTLRSNAQROEISAAPKTLFGRLDLDLXSE 48
Db 32 KAMKGLTDEESITLTLRSNAQROEISAAPKTLFGRLDLDLXSE 78

RESULT 14

US-09-925-297-479
Sequence 479, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 479
LENGTH: 158

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (66)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match 57.6%; Score 133; DB 9; Length 158;
Best Local Similarity 47.9%; Pred. No. 1e-10;
Matches 23; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

Qy 1 RKAMKGLTDEESITLTLRSNAQROEISAAPKTLFGRLDLDLXSE 48
Db 39 QKAIKIGTDEKMLITLTLRSNAQROEISAAPKTLFGRLDLDLXSE 86

RESULT 15

US-10-205-823-34
Sequence 34, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.

APPLICANT: Endege, Wilson O.
APPLICANT: Ganavarapu, Manjula

APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian

APPLICANT: Kamakar, Shubhangi
APPLICANT: Womey, Angela M.

APPLICANT: Gialt, Karen
APPLICANT: Zhao, Xumei

APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-34

Query Match 56.7%; Score 131; DB 14; Length 323;
Best Local Similarity 47.9%; Pred. No. 4.9e-10;
Matches 23; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

Qy 1 RKAMKGLTDEESITLTLRSNAQROEISAAPKTLFGRLDLDLXSE 48
Db 28 QKAIKIGTDEKMLITLTLRSNAQROEISAAPKTLFGRLDLDLXSE 75

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GenCore version 5.1.6
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March 25, 2004, 08:05:00 ; Search time 46 Seconds
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Maximum Match 100%
Listing first 100 summaries

Published Applications AA:**

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
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as derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	DB	ID	Description
1600	100.0	320	13	US-10-007-761-72	Sequence 72, Appl
600	100.0	320	16	US-10-424-232-1	Sequence 1, Appli
590	99.4	327	9	US-09-970-969-2	Sequence 2, Appli
590	99.4	327	9	US-09-970-969-4	Sequence 4, Appli
590	99.4	327	9	US-09-970-969-6	Sequence 6, Appli
1.5	90.7	319	14	US-10-080-370-3	Sequence 3, Appli
1.5	90.7	669	14	US-10-080-370-6	Sequence 6, Appli
012	63.2	208	9	US-09-925-302-731	Sequence 731, Appl
933	58.3	321	14	US-10-097-340-10	Sequence 10, Appl
933	58.3	324	9	US-09-925-301-1062	Sequence 1062, Ap
927	57.9	675	12	US-10-114-270-160	Sequence 160, App
2.5	52.0	327	15	US-10-236-031B-18	Sequence 18, Appl
811	50.7	323	14	US-10-205-823-34	Sequence 34, Appl
781	48.8	324	14	US-10-316-253-262	Sequence 262, Appl
780	48.8	485	9	US-09-925-300-1664	Sequence 1664, Ap

16	708.5	44.3	339	9	US-09-974-298-91	Sequence 91, Appl
17	708.5	44.3	339	14	US-10-097-340-6	Sequence 6, Appli
18	708.5	44.3	339	14	US-10-097-340-8	Sequence 8, Appli
19	683	42.7	327	9	US-09-764-853-615	Sequence 615, App
20	680	42.5	332	10	US-09-764-881-110	Sequence 110, App
21	680	42.5	332	15	US-10-242-747-110	Sequence 110, App
22	658.5	41.2	319	14	US-10-304-287-2	Sequence 2, Appli
23	653	40.8	373	9	US-09-925-301-888	Sequence 888, App
24	653	40.8	388	12	US-10-276-774-2250	Sequence 2250, Ap
25	649	40.6	346	9	US-09-919-172-39	Sequence 39, Appl
26	649	40.6	346	9	US-09-974-298-93	Sequence 93, Appl
27	642	40.1	346	14	US-10-316-253-300	Sequence 300, App
28	581.5	36.3	322	15	US-10-369-493-5717	Sequence 5717, Ap
29	540	33.8	317	15	US-10-369-493-5695	Sequence 5695, Ap
30	511	31.9	364	12	US-10-425-114-59570	Sequence 59570, A
31	511	31.9	369	12	US-10-425-114-66547	Sequence 66547, A
32	510	31.9	330	12	US-10-425-114-61774	Sequence 61774, A
33	502	31.4	329	12	US-10-425-114-63278	Sequence 63278, A
34	500.5	31.3	326	12	US-10-424-599-257117	Sequence 257117,
35	481.5	30.1	327	12	US-10-425-114-52360	Sequence 52360, A
36	469.5	29.3	322	12	US-10-424-599-196945	Sequence 196945,
37	431	26.9	313	12	US-10-424-599-279849	Sequence 279849,
38	431	26.9	320	12	US-10-425-114-55270	Sequence 55270, A
39	431	26.9	324	12	US-10-425-114-43962	Sequence 43962, A
40	430.5	26.9	314	12	US-10-424-599-279847	Sequence 279847,
41	410.5	25.7	304	12	US-10-424-599-231427	Sequence 231427,
42	408.5	25.5	312	12	US-10-424-599-172904	Sequence 172904,
43	405.5	25.3	320	12	US-10-424-599-201908	Sequence 201908,
44	401.5	25.1	316	12	US-10-424-599-144032	Sequence 144032,
45	401.5	25.1	333	12	US-10-425-114-47663	Sequence 47663, A
46	401.5	25.1	333	12	US-10-425-114-55802	Sequence 55802, A
47	399.5	25.0	289	9	US-09-925-301-897	Sequence 897, App
48	398.5	24.9	314	12	US-10-424-599-273745	Sequence 273745,
49	393.5	24.6	319	12	US-10-424-599-213299	Sequence 213299,
50	388	24.2	173	12	US-10-424-599-203868	Sequence 203868,
51	387	24.2	518	15	US-10-369-493-3240	Sequence 3240, Ap
52	384.5	24.0	339	12	US-10-425-114-60631	Sequence 60631, A
53	384.5	24.0	361	12	US-10-425-114-64727	Sequence 64727, A
54	384	24.0	181	15	US-10-104-047-2800	Sequence 2800, Ap
55	382.5	23.9	341	12	US-10-425-114-60513	Sequence 60513, A
56	382.5	23.9	344	12	US-10-425-114-59289	Sequence 59289, A
57	382	23.9	319	12	US-10-424-599-230318	Sequence 230318,
58	382	23.9	449	15	US-10-369-493-12408	Sequence 12408, A
59	381.5	23.8	316	14	US-10-219-220-260	Sequence 260, App
60	378.5	23.7	316	14	US-10-219-220-62	Sequence 62, Appl
61	378.5	23.7	316	15	US-10-393-840-56	Sequence 56, Appl
62	378.5	23.7	316	15	US-10-369-493-6310	Sequence 6310, Ap
63	370	23.1	351	15	US-10-425-114-40052	Sequence 40052, A
64	347.5	21.7	333	12	US-10-369-493-13195	Sequence 13195, A
65	336.5	21.0	158	9	US-09-925-297-479	Sequence 479, App
66	334.5	20.9	322	15	US-10-369-493-13195	Sequence 13195, A
67	332	20.8	213	15	US-10-393-840-53	Sequence 53, Appl
68	284.5	17.8	245	12	US-10-425-114-43123	Sequence 43123, A
69	284.5	17.8	270	12	US-10-424-599-211315	Sequence 211315,
70	274	17.1	333	12	US-10-425-114-72654	Sequence 72654, A
71	273.5	17.1	212	12	US-10-425-114-68027	Sequence 68027, A
72	265.5	16.6	242	15	US-10-393-840-55	Sequence 55, Appl
73	257.5	16.1	241	12	US-10-425-114-41196	Sequence 41196, A
74	245.5	15.3	239	14	US-10-219-220-65	Sequence 65, Appl
75	245.5	15.3	239	15	US-10-393-840-54	Sequence 54, Appl
76	245.5	15.3	239	15	US-10-393-840-117	Sequence 117, App
77	232	14.5	184	14	US-10-219-220-66	Sequence 66, Appl
78	232	14.5	184	15	US-10-393-840-118	Sequence 118, App
79	229	14.3	112	15	US-10-264-049-3741	Sequence 3741, Ap
80	222	13.9	184	15	US-10-393-840-52	Sequence 52, Appl
81	221	13.8	319	14	US-10-259-165-56	Sequence 56, Appl
82	221	13.8	319	14	US-10-259-165-402	Sequence 402, App
83	219	13.7	81	12	US-10-424-599-271482	Sequence 271482,
84	214.5	13.4	336	14	US-10-259-165-290	Sequence 290, App
85	184.5	11.5	177	12	US-10-424-599-186704	Sequence 186704,
86	184	11.5	186	15	US-10-264-049-2936	Sequence 2936, Ap
87	161.5	10.1	142	12	US-10-424-599-201914	Sequence 201914,
88	150	9.4	100	12	US-10-424-599-223868	Sequence 223868,

Sequence 951, App
Sequence 71353, A
Sequence 198302,
Sequence 279848,
Sequence 1467, Ap
Sequence 243530,
Sequence 30160, A
Sequence 952, App
Sequence 160681,
Sequence 63, App1
Sequence 115, App
Sequence 3937, Ap

ALIGNMENTS

RESULT 1
US-10-007-761-72
; Sequence 72, Application US/10007761
; Publication No. US20020150984A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: Peptides for Activation and Inhibition
; FILE OF INVENTION: of delta-PKC
; FILE REFERENCE: 58600-8208.US00
; CURRENT APPLICATION NUMBER: US/10/007,761
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/262,060
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-761-72

Query Match 100.0%; Score 1600; DB 13; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.6e-139;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPPGDFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAFAKTL 60
DB 1 MAQVLRGTVDPPGDFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAFAKTL 60
QY 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
DB 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 121 ELRAIKQVYEEYGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
DB 121 ELRAIKQVYEEYGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
QY 181 QAGELKWTGDEKFTIFGTRSVSHLRKVDFKYMVTISGFOIETIDRETSGNLEQLLAV 240
DB 181 QAGELKWTGDEKFTIFGTRSVSHLRKVDFKYMVTISGFOIETIDRETSGNLEQLLAV 240
QY 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
DB 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
QY 301 KGDTSQDYKALLLCGEDD 320
DB 301 KGDTSQDYKALLLCGEDD 320

RESULT 2
US-10-424-232-1
; Sequence 1, Application US/10424232
; Publication No. US20040022731A1
; GENERAL INFORMATION:
; APPLICANT: Bogdanov, Alexei

APPLICANT: Schellenberger, Eyk
APPLICANT: Petrovsky, Alexander
APPLICANT: Jcsephson, Lee
TITLE OF INVENTION: In vivo Imaging of Apoptosis
FILE REFERENCE: 00786-549001
CURRENT APPLICATION NUMBER: US/10/424,232
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/60/376,052
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-424-232-1

Query Match 100.0%; Score 1600; DB 16; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.6e-139;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPPGDFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAFAKTL 60
DB 1 MAQVLRGTVDPPGDFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAFAKTL 60
QY 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
DB 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 121 ELRAIKQVYEEYGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
DB 121 ELRAIKQVYEEYGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
QY 181 QAGELKWTGDEKFTIFGTRSVSHLRKVDFKYMVTISGFOIETIDRETSGNLEQLLAV 240
DB 181 QAGELKWTGDEKFTIFGTRSVSHLRKVDFKYMVTISGFOIETIDRETSGNLEQLLAV 240
QY 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
DB 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
QY 301 KGDTSQDYKALLLCGEDD 320
DB 301 KGDTSQDYKALLLCGEDD 320

RESULT 3
US-09-970-969-2
; Sequence 2, Application US/09970969
; Patent No. US20020103341A1
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan F.
; APPLICANT: Erown, David S.
; TITLE OF INVENTION: Amexin Derivatives with Endogenous Chelation Sites
; FILE REFERENCE: uofw-1-13841
; CURRENT APPLICATION NUMBER: US/09/970,969
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-969-2

Query Match 99.4%; Score 1590; DB 9; Length 327;
Best Local Similarity 99.7%; Pred. No. 2.2e-138;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPPGDFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAFAKTL 60
DB 8 MAQVLRGTVDPPGDFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAFAKTL 67

1	FGRDLLDDLKSELTGKFEKLIVALMKP	SRLYDAYELXHALKGAGTNEKVLTEIIASRTPE	120
8	FGRDLLDDLKSELTGKFEKLIVALMKP	SRLYDAYELXHALKGAGTNEKVLTEIIASRTPE	127
1	ELRAIKQVVEEYEGSSLEDDVGDTSGYYQRM	VVLQANRDPDAGIDEAQVEDQAQLF	180
8	ELRAIKQVVEEYEGSSLEDDVGDTSGYYQRM	VVLQANRDPDAGIDEAQVEDQAQLF	187
1	QAGELKWGTDEEKFIITIGTRSVSHLRKVFDKYMTISGFQI	EETIDRETSGNLEQLLAV	240
8	QAGELKWGTDEEKFIITIGTRSVSHLRKVFDKYMTISGFQI	EETIDRETSGNLEQLLAV	247
1	VKSIRSIIPAYLAETLYYAMKGAGTDHHTLIRVMVSRSEIDL	FNIRKEFRKNFATSLYSMI	300
8	VKSIRSIIPAYLAETLYYAMKGAGTDHHTLIRVMVSRSEIDL	FNIRKEFRKNFATSLYSMI	307
1	KGDTSGDYKKALLILCGEDD	320	
8	KGDTSGDYKKALLILCGEDD	327	
9-4	Application US/09970969		
1	US20020103341A1		
INFORMATION:			
Inventor:	Tait, Jonathan P.		
Attorney:	Brown, David S.		
INVENTION:	Annexin Derivatives with Endogenous Chelation Sites		
REFERENCE:	wof-1-13841		
APPLICATION NUMBER:	US/09/970,969		
FILING DATE:	2001-10-03		
PATENT ID NOS:	6		
Patent In Ver.	2.0		
4			
327			
XT			
9-4	Homo sapiens		
ch	99.4%; Score 1590; DB 9: Length 327;		
l Similarity	99.7%; Pred. No. 2.2e-138;		
919; Conservative	0; Mismatches 1; Indels 0; Gaps 0		
1	MAQVLRGTVDTPGGFERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAFAFKTL	60	
8	MAQVLRGTVDTPGGFERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAFAFKTL	67	
1	FGRDLLDDLKSELTGKFEKLIVALMKP	SRLYDAYELXHALKGAGTNEKVLTEIIASRTPE	120
8	FGRDLLDDLKSELTGKFEKLIVALMKP	SRLYDAYELXHALKGAGTNEKVLTEIIASRTPE	127
1	ELRAIKQVVEEYEGSSLEDDVGDTSGYYQRM	VVLQANRDPDAGIDEAQVEDQAQLF	180
8	ELRAIKQVVEEYEGSSLEDDVGDTSGYYQRM	VVLQANRDPDAGIDEAQVEDQAQLF	187
1	QAGELKWGTDEEKFIITIGTRSVSHLRKVFDKYMTISGFQI	EETIDRETSGNLEQLLAV	240
8	QAGELKWGTDEEKFIITIGTRSVSHLRKVFDKYMTISGFQI	EETIDRETSGNLEQLLAV	247
1	VKSIRSIIPAYLAETLYYAMKGAGTDHHTLIRVMVSRSEIDL	FNIRKEFRKNFATSLYSMI	300
8	VKSIRSIIPAYLAETLYYAMKGAGTDHHTLIRVMVSRSEIDL	FNIRKEFRKNFATSLYSMI	307
1	KGDTSGDYKKALLILCGEDD	320	
8	KGDTSGDYKKALLILCGEDD	327	
9-6	Application US/09970969		
6,	US20020103341A1		

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; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan F.
; APPLICANT: Brown, David S.
; TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
; FILE REFERENCE: uofw-1-13841
; CURRENT APPLICATION NUMBER: US/09/970,969
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-970-969-6

Query Match          99.4%; Score 1590; DB 9; Length 327;
Best Local Similarity 99.7%; Pred. No. 2.2e-138;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDDEESILTLTSRSNAQRQEISAAFKTL 60
DB 8 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDDEESILTLTSRSNAQRQEISAAFKTL 67
QY 61 FGRDLLDLKSELTKGFEKLIVALKMPSRLVDAYELKHALKGAGTNEKVLTEIIASRTPE 120
DB 68 FGRDLLDLKSELTKGFEKLIVALKMPSRLVDAYELKHALKGAGTNEKVLTEIIASRTPE 127
QY 121 ELRAIKQVBEYEGSSLEDDVVGDTSGYYQYRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
DB 128 ELRAIKQVBEYEGSSLEDDVVGDTSGYYQYRMVLVLLQANRPDAGIDEAQVEQDAQALF 187
QY 181 QAGELKWTGDEBKETITFGTSSVSHLRKVFQDKYMTISGQIEETIDRETSGNLEQLLLAV 240
DB 188 QAGELKWTGDEBKETITFGTSSVSHLRKVFQDKYMTISGQIEETIDRETSGNLEQLLLAV 247
QY 241 VKSIRSPAYLAETLYAMKAGAGTDDHTLIRVWVSERSEIDLFNIRKEFRKNFATSLYSMI 300
DB 248 VKSIRSPAYLAETLYAMKAGAGTDDHTLIRVWVSERSEIDLFNIRKEFRKNFATSLYSMI 307
QY 301 KGDTSGDYKXKALLLCGEDD 320
DB 308 KGDTSGDYKXKALLLCGEDD 327

RESULT 6
US-10-080-370-3
; Sequence 3, Application US/10080370
; Publication No. US20030166532A1
; GENERAL INFORMATION:
; APPLICANT: Allison, Anthony
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
; FILE REFERENCE: SUER.90
; CURRENT APPLICATION NUMBER: US/10/080,370
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,402
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/332,582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-080-370-3

Query Match          90.7%; Score 1451.5; DB 14; Length 319;
Best Local Similarity 91.5%; Pred. No. 1.3e-125;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 5 LRGTVTDPFGFDERADAETLRKAMKGLGTDDEESILTLTSRSNAQRQEISAAFKTLFGDR 64
DB 3 LRGTVTDPFGFDERADAETLRKAMKGLGTDDEESILTLTSRSNAQRQEISAAFKTLFGDR 62

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QY 65 LDDKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
Db 63 LVNDKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRA 122
QY 125 IKQVVEEYEGSLEDVVGDTSGYYQRMVLLVLLQANRPDAGIDEAQVEQDAALFQAGE 184
Db 123 IKQVVEEYEGSLEDVVGDTSGYYQRMVLLVLLQANRPDAGIDEAQVEQDAALFQAGE 182
QY 185 LKMGTDDEKFIITIGTRSVSHLRKVPDKYMTISGFIQIETIDRETSGNLEQLLLAVVXSI 244
Db 183 LKMGTDDEKFIITIGTRSVSHLRKVPDKYMTISGFIQIETIDRETSGNLEQLLLAVVXSI 242
QY 245 RSIPLAETLYYAMKAGTDHDTLIRVMSRSEIDLNFIRKPKNFATSLYSIMIKGDT 304
Db 243 RSIPLAETLYYAMKAGTDHDTLIRVMSRSEIDLNFIRKPKNFATSLYSIMIKGDT 302
QY 305 SGDYKALLLLC-GEED 320
Db 303 SGDYKALLLLC-GEED 319

RESULT 7
US-10-080-370-6
; Sequence 6, Application US/10080370
; Publication No. US20030166532A1
; GENERAL INFORMATION:
; APPLICANT: Allison, Anthony
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
; FILE REFERENCE: SURR.90
; CURRENT APPLICATION NUMBER: US/10/080,370
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,402
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/332,582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
; NAME/KEY: misc feature
; LOCATION: (334)..(334)
; OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; OTHER INFORMATION: modified annexin gene
; NAME/KEY: misc feature
; LOCATION: (45)..(45)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (1000)..(1002)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (1051)..(1053)
; OTHER INFORMATION: n = a, c, g, or t
US-10-080-370-6

Query Match 90.7%; Score 1451.5; DB 14; Length 669;
Best Local Similarity 91.5%; Pred. No. 3.9e-125;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 5 LGRTVTFPGFDERADAETLRKMKGLGTDEESILTLTSSNAQRQEISAAFKTLFGRD 64

Db 17 LGRTVTFPGFDERADAETLRKMKGLGTDEESILTLTSSNAQRQEISAAFKTLFGRD 76
QY 65 LDDKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
Db 77 LVNDKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRA 136
QY 125 IKQVVEEYEGSLEDVVGDTSGYYQRMVLLVLLQANRPDAGIDEAQVEQDAALFQAGE 184
Db 137 IKQVVEEYEGSLEDVVGDTSGYYQRMVLLVLLQANRPDAGIDEAQVEQDAALFQAGE 196
QY 185 LKMGTDDEKFIITIGTRSVSHLRKVPDKYMTISGFIQIETIDRETSGNLEQLLLAVVXSI 244
Db 197 LKMGTDDEKFIITIGTRSVSHLRKVPDKYMTISGFIQIETIDRETSGNLEQLLLAVVXSI 256
QY 245 RSIPLAETLYYAMKAGTDHDTLIRVMSRSEIDLNFIRKPKNFATSLYSIMIKGDT 304
Db 257 RSIPLAETLYYAMKAGTDHDTLIRVMSRSEIDLNFIRKPKNFATSLYSIMIKGDT 316
QY 305 SGDYKALLLLC-GEED 320
Db 317 SGDYKALLLLC-GEED 333

RESULT 8
US-09-925-302-731
; Sequence 731, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 731
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-731

Query Match 63.2%; Score 1012; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.8e-85;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQVLRGTVTFPGFDERADAETLRKMKGLGTDEESILTLTSSNAQRQEISAAFKTL 60
Db 4 MAQVLRGTVTFPGFDERADAETLRKMKGLGTDEESILTLTSSNAQRQEISAAFKTL 63
QY 61 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
Db 64 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 123
QY 121 ELRAIKQVVEEYEGSLEDVVGDTSGYYQRMVLLVLLQANRPDAGIDEAQVEQDAALF 180
Db 124 ELRAIKQVVEEYEGSLEDVVGDTSGYYQRMVLLVLLQANRPDAGIDEAQVEQDAALF 183
QY 181 QAGELKMGTDDEKFIITIGTRSV 203
Db 184 QAGELKMGTDDEKFIITIGTRSV 206

RESULT 9
US-10-097-340-10
; Sequence 10, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN

```
WT: Manjula GANNAVARAPU
T: Sebastian HOERSCH
T: Shubhangi KAMATKAR
T: Steve G. KOVATS
T: Rachel E. MEYERS
WT: Michael MORRISSEY
WT: Peter OLANDT
WT: Ami SEN
WT: Peter VEIBY
WT: Gordon B. MILLS
WT: Robert C. BAST, Jr.
T: Karen LU
WT: Rosemarie SCHMANDT
T: Xumei ZHAO
WT: Karen GLATT
INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
           Assessment, Prevention, and Therapy of Ovarian Cancer
REFERENCE: MRI-030
APPLICATION NUMBER: US/10/097,340
FILING DATE: 2002-03-14
PPLICATION NUMBER: 60/276,025
LING DATE: 2001-03-14
PLICATION NUMBER: 60/325,149
LING DATE: 2001-09-26
PLICATION NUMBER: 60/276,026
LING DATE: 2001-03-14
PLICATION NUMBER: 60/324,967
LING DATE: 2001/09/26
PLICATION NUMBER: 60/311,732
LING DATE: 2001-08-10
PLICATION NUMBER: 60/325,102
LING DATE: 2001-09-26
PLICATION NUMBER: 60/323,580
LING DATE: 2001-09-19
F SEQ ID NOS: 363
: FastSEQ for Windows Version 4.0
10
10
321
RT
M: Homo sapiens
40-10
ch 58.3%; Score 933; DB 14; Length 321;
1 Similarity 58.6%; Pred. No. 1e-77;
184; Conservative 53; Mismatches 77; Indels 0; Gaps 0;
7 GTVTDPFGDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEISAFAFKTLFGCDLL 66
8 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAQOEIRTAAYKSTIGRDLI 67
67 DLLKSELTKFKEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
68 DLLKSELSCNFEQIVGMMPTTVLYDVQELRRAMKAGTDEGCLIEILASRTPEEIRIS 127
27 QVVEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQAGELK 186
28 QTVQQQYGRSLEDDIRSDFSMFQVRLVLSAGRDEGNVLDALVRQDAQDLYEAGEKK 187
87 WGTDEEKFTIFGTRSVSHLRKVDFKMYMTISGQIEBTIDRETSGNLEQLLLAVVKSIRS 246
88 WGTDEVKFLTVLCNRNHLHVFDEYKRIQDKIEQSIKSETSGSFEDALLAIVKCMRN 247
47 IPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFIRKFNKFNATSLYSMIKGDTS 306
48 KSAYFAEKLYKSMKGLGTDDNTLIRVWVSRAEIDMLDIRAHFKRLYKSLYSFIKGDTS 307
07 DYKALLLLCGEDD 320
08 DYRKVLLVLCGGDD 321
01-1062
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; Sequence 1062, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1062
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1062
Query Match 58.3%; Score 933; DB 9; Length 324;
Best Local Similarity 58.6%; Pred. No. 1.e-77;
Matches 184; Conservative 53; Mismatches 77; Indels 0; Gaps 0;
QY 7 GTVTDPFGDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEISAFAFKTLFGCDLL 66
DB 11 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAQOEIRTAAYKSTIGRDLI 70
QY 67 DLLKSELTKFKEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
DB 71 DLLKSELSCNFEQIVGMMPTTVLYDVQELRRAMKAGTDEGCLIEILASRTPEEIRIS 130
QY 127 QVVEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQAGELK 186
DB 131 QTVQQQYGRSLEDDIRSDFSMFQVRLVLSAGRDEGNVLDALVRQDAQDLYEAGEKK 190
QY 187 WGTDEEKFTIFGTRSVSHLRKVDFKMYMTISGQIEBTIDRETSGNLEQLLLAVVKSIRS 246
DB 191 WGTDEVKFLTVLCNRNHLHVFDEYKRIQDKIEQSIKSETSGSFEDALLAIVKCMRN 250
QY 247 IPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFIRKFNKFNATSLYSMIKGDTS 306
DB 251 KSAYFAEKLYKSMKGLGTDDNTLIRVWVSRAEIDMLDIRAHFKRLYKSLYSFIKGDTS 310
QY 307 DYKALLLLCGEDD 320
DB 311 DYRKVLLVLCGGDD 324
RESULT 11
US-10-114-270-160
; Sequence 160, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Rekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziaohong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glennnda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
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; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liette, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids. Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2001-04-10
; PRIOR FILING DATE: 2001-04-10
; PRIOR FILING DATE: 2001-04-10
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 160
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-114-270-160

Query Match      57.9%; Score 927; DB 12; Length 675;
Best Local Similarity 57.8%; Pred. No. 1.1e-76;
Matches 182; Conservative 52; Mismatches 81; Indels 0; Gaps 0;

QY      6  RGTVTDFPGFDERADAEATLRKAMKGLTGDEESILTLTSRSNAQRQEISAAPKTLFGRDL 65
Db      11  RGSIHDFPGFDPQDAEALYATAMKFGSDKEAILDIITSRNQRQEVQCSYKSLYKDL 70

QY      66  LDDLKSELTKPEKLIIVALKMPSRLYDAYELHAKLGAGTNEKVLTEIIASRTPBELRAI 125
Db      71  IADLKVELTKPEKLIIVGLMRPVPAYCDAKEIKDAISGIGTDEKCLIEILASRTNEQMHL 130

QY      126  KOVVEEYGSLEDDVVGTSYQYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185
Db      131  VAAKYDAVERDLEADIIIGTSGHGFQKMLVLLQGTREDDVVSDELVOQDQVLYEAGEL 190

QY      186  KGTDEEKFITTFGRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKSIR 245
Db      191  KNGTDEAQFIYILGNRSKQHLRFDYELTKTKPIEASIRGELSGDFEKLMLAVVKCIR 250

QY      246  SIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 305
Db      251  STPEFAERLFAKMGKLGTRDNLIRIMVSRSEIDLNLKCHFKMYGKTLSSMIMEDTSG 310

QY      306  GDYKALLLGGEDD 320
Db      311  GEYKTKLLKSGDD 325

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; RESULT 12
```

```
US-10-236-031B-18
; Sequence 18, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, Gavin J.
; APPLICANT: Jensen, Roderick V.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236,031B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,389
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/407,431
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-236-031B-18

Query Match      52.0%; Score 832.5; DB 15; Length 327;
Best Local Similarity 56.5%; Pred. No. 2.1e-68;
Matches 177; Conservative 48; Mismatches 87; Indels 1; Gaps 1;

QY      8  TVTDFPGFDERADAEATLRKAMKGLTGDEESILTLTSRSNAQRQEISAAPKTLFGRDL 67
Db      14  TVKSSSHFNPDPAETLYKAMKGIGTNEQAIDVLTKESNTQRQIAKSFKAQFGKDLTE 73

QY      68  DLKSELTKPEKLIIVALKMPSRLYDAYELHAKLGAGTNEKVLTEIIASRTPBELRAIKQ 127
Db      74  TLKSELGKPEKLIIVALKMPPRYEAKELHDMKGLTGKEGVIIILASRTKNQLREIMK 133

QY      128  VVEEYGSLEDDVVGTSYQYQRMVLVLLQANRDP-DAGIDEAQVEQDAQALFOAGELK 186
Db      134  AYEEDYGSLEDDIQADTSGYLERILVCLLQGRDDVSSFVDPALALQADQLVAAAGSKI 193

QY      187  WGTDEEKFITTFGRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKSIRS 246
Db      194  RGTDEMKFITTLCTRSAATHLLRVFEEYKIAKNSIEDSIKSETHGSLSEAMLTVVVKCTQN 253

QY      247  IPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 306
Db      254  LHSFPAERLYYAMKAGAGTRDGLTIRNIVSRSEIDLNLKCHFKMYGKTLSSMIMEDTSG 313

QY      307  DYKALLLGGED 319
Db      314  DYKNALLSLVGS 326
```

RESULT 13

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US-10-205-823-34
; Sequence 34, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: McNahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Heerssch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
```

APPLICATION NUMBER: US/10/205,823
FILING DATE: 2002-07-25
APPLICATION NUMBER: 60/307,982
LING DATE: 2001-07-25
APPLICATION NUMBER: 60/314,356
LING DATE: 2001-08-22
APPLICATION NUMBER: 60/325,020
LING DATE: 2001-09-25
APPLICATION NUMBER: 60/341,746
LING DATE: 2001-12-12
APPLICATION NUMBER: 60/362,158
LING DATE: 2002-03-05
F SEQ ID NOS: 455
F SEQ ID NOS: 455
FAST-SEQ for Windows Version 4.0
323
323

RT
M: Homo sapiens

ch

50.7%; Score 811; DB 14; Length 323;
1 Similarity 50.2%; Pred. No. 2e-66;
158; Conservative 61; Mismatches 96; Indels 0; Gaps 0;

6 RGTVPDPGDERADAEATLRKAMKGLGTDEESILTLTSSNAQORQISAAFKTLFGDRL 65

9 RGVTRDYPDPSPVDAEAIKAKIGTDEKTLNLTSSNAQORQISAAFKTLFGDRL 68

66 LDLKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125

69 KDLKGLDLSGHFELHVALVTPPAVFDKQKSKMGAGTNEDEALTEILTRTSRQMKDI 128

26 KQYEEYSGSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 185

29 SQAYTYTVYKSLGDISSETSGDFRKALLTLADGRDESILKVDHLAKDAQILYKAGEN 188

86 KWTDEKFTITIGTRSVSHLRKVPDKYMTISQFIEETIDRETSGNLEQLLAVVKSIR 245

89 RWGTDEKFTTEILCLRSFPQKLTDFEYRNISQKDIEDSIKGLSGHFEDLLLAIVNCVR 248

46 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNIKEFRKNPATSLYSMIKGDTS 305

49 NTPAFLAERLHRAKLGIGTDEFTLNRMVSRSEIDLNIKEFRKNPATSLYSMIKGDTS 308

06 GDYKKAALLLCGGDD 320

09 GDYEITLLKICGGDD 323

53-262

262, Application US/10316253
on No. US20030162706A1

INFORMATION:

T: The Procter & Gamble Company

T: Peters, Kevin

T: Thompson, Larry

T: Wang, Feng

T: Greis, Kenneth

INVENTION: Angiogenesis Modulating Proteins

ERENCE: 8865M

APPLICATION NUMBER: US/10/316,253

FILING DATE: 2002-12-10

PLICATION NUMBER: US 60/355,295

LING DATE: 2002-02-08

F SEQ ID NOS: 308

F SEQ ID NOS: 308

262

324

RT

M: Rattus norvegicus

53-262

Query Match 48.8%; Score 781; DB 14; Length 324;
Best Local Similarity 48.3%; Pred. No. 1.2e-63;
Matches 152; Conservative 64; Mismatches 99; Indels 0; Gaps 0;

QY 6 RGTVPDPGDERADAEATLRKAMKGLGTDEESILTLTSSNAQORQISAAFKTLFGDRL 65

Db 10 RGTINYPGPNVSDAEAIKAKIGTDEKTLNLTSSNAQORQISAAFKTLFGDRL 69

QY 66 LDLKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125

Db 70 KADLKGDLSGHFELHVALVTPPAVFDKQKSKMGAGTNEDEALTEILTRTSRQMKDI 129

QY 126 KQYEEYSGSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 185

Db 130 SQAYTYTVYKSLGDISSETSGDFRKALLTLADGRDESILKVDHLAKDAQILYKAGEN 189

QY 186 KWTDEKFTITIGTRSVSHLRKVPDKYMTISQFIEETIDRETSGNLEQLLAVVKSIR 245

Db 190 KWTDEKFTTEILCLRSFPQKLTDFEYRNISQKDIEDSIKGLSGHFEDLLLAIVNCVR 249

QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNIKEFRKNPATSLYSMIKGDTS 305

Db 250 NTPAFLAERLHRAKLGIGTDEFTLNRMVSRSEIDLNIKEFRKNPATSLYSMIKGDTS 309

QY 306 GDYKKAALLLCGGDD 320

Db 310 GDYEITLLKICGGDD 324

RESULT 15

US-09-925-300-1664

; Sequence 1664, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1664

; LENGTH: 485

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-925-300-1664

Query Match 48.8%; Score 780; DB 9; Length 485;
Best Local Similarity 48.1%; Pred. No. 2.6e-63;
Matches 153; Conservative 66; Mismatches 99; Indels 0; Gaps 0;

QY 1 MAQVLRTGVTDPGDERADAEATLRKAMKGLGTDEESILTLTSSNAQORQISAAFKTL 60

Db 168 VTQVTQGTIRPAANFDAIRDAEILRKAMKGFQDEQAIYDVVVRNSNDQKIKAAFKTS 227

QY 61 FGRDLLDLKSELTKGFKELI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

Db 228 YGKDLIKDLKSELSGNMEELIALFMPPTYYDAWSLRKAMQAGTQERVLEILCTRINQ 287

QY 121 ELRAIKQVEEYSGSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 180

Db 288 EIREIVRCYQSEFGRDLEKDIIRSDTSGHFERLLVSMCQGNROENQINHQMAQEDARLY 347

QY 181 QAQELKWTGDEEKFTITIGTRSVSHLRKVPDKYMTISQFIEETIDRETSGNLEQLLAV 240

Db 348 QAQEGRLGTDSCFNWILATRSFPQURATMEAYSRVANDLLSSVSREFSGYVESGLKTI 407

QY 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNIKEFRKNPATSLYSMI 300

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db      408  LQCALNRPFAERLYYAMKAGTDDSTLVRIVTVTRSEIDLVIQKQFAQMYOKTLGTMI 467
Qy      301  KGDTSGDYKKALLLCGE 318
Db      468  AGDTSGDYRRLLLAIVGQ 485

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RESULT 16
US-09-974-298-91
; Sequence 91, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 91
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO. US20020156263A1 13
US-09-974-298-91

```

Query Match	44.3%;	Score	708.5;	DB	9;	Length	339;
Best Local Similarity	46.3%;	Pred. No.	6.2e-57;				
Matches	146;	Conservative	63;	Mismatches	105;	Indels	1;
Gaps	1;						
Qy	7	GTVTDFPGFDRADAETLRKAMKGLGTDDEESILTLTSSRNAQOEISAAFKTLGFRDLL	66				
Db	25	GSVKAYTNFDAERDALNIETAIKTGVDDEVITVILTLNRSNAQODIAFAYQRRTKELA	84				
Qy	67	DDLKSELTKGPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEITASTPEELRAIK	126				
Db	85	SALKSALSGLHLETWILGLTKTPAQDASELAKSMKGLGTDEDSLTEIILCSRTNOELQIN	144				
Qy	127	QVYEEYCGSSLEDDVVGDTSGYVQRMVLVLQANRPDAG-IDEAQVQDAQALFQAGEL	185				
Db	145	RVYKEMYKTDLKEDIISPTSGDGRKLIMVALAKGRAEDGSVIDELIDQDARDLYDAGVK	204				
Qy	186	KWGTDEEKFIITFGTRSYSHLRKVPDKYMTLTSGFOIETITDRETSNGLEQLLAVVKIR	245				
Db	205	RKGTDPVKWIIMTTERSYPHLQKVPDRYKSYSPYDMLSEIRKEVKGDLNENFLNLVQCII	264				
Qy	246	SIPAYLAETLYAMKAGTDDHTLIRVMVSSEIDLFNIRKEFRKNFATSLYSMTIKGDT	305				
Db	265	NKPLYFADRLYDSMKGKGRDKVLIRIMVSRSEVDMLKIRSEFKRYKSLYYITQDDTK	324				
Qy	306	GDYKCALILLCCGEDD	320				
Db	325	GDYKALLYLCGGDD	339				

RESULT 17
US-10-097-340-6
; Sequence 6, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVARS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISBY
; APPLICANT: Peter OLANDT

```

; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. EAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; IS-10-097-340-6

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Query Match	44.3%;	Score	708.5;	DB	14;	Length	339;	
Best Local Similarity	46.3%;	Pred. No.	6.2e-57;					
Matches	146;	Conservative	63;	Mismatches	105;	Indels	1;	
							Gaps	1;
Qy	7	GTVTDFPGFPERADAETLRKAMKGLGTDEBSILTLT	SRSNAOQETSA	AAFKTLT	FGRLDL	66		
Db	25	GSVKAYTNFDAERDALNIETAIKGTGVDEVITVNI	LTRSNAOQDIA	FAYORRTK	KELA	84		
Qy	67	DDLKSELTGFEKLI VALMKPSRILYDAYELKHAL	KAGTNEKVI	TEII	ASTTPEEL	RAIK	126	
Db	85	SAIKSAISGHLTETVILGLKTPAQYDASEL	KAMKGLGT	DEDS	ETI	ICS	TNOELQ	144
Qy	127	QVTEEEYGSSLEDDVVGDTSGYYORMVLVLL	QANRDP	DPA	G	IDEA	QVEOD	185
Db	145	RVTKEMYKTDLKDIISDTSGDFPKMVALAK	GRAEDG	SV	VIDEL	IDQ	DARDLY	204
Qy	186	KWGTDEEKFITIGTRSVSHLRKVPFDKYMTIS	GFQI	ETI	DRETSG	NLEQL	LAVVK	245
Db	205	RKGTDPVKWISIMTSPVPHLQKVFDRYKSY	SPYDML	ESTIR	KEVKG	DLEN	AFNLV	264
Qy	246	SIPAYLAETLYAMKAGTDHDTLIRVMVSR	SEIDL	FNIR	KEKRN	FAT	SLYS	305
Db	265	NKPLYFADRLYDSMKGRGTRDKVILIR	MSRSEV	DML	KIRSE	FRK	YKGS	324
Qy	306	GDYKKA	LLLC	GDD				
Db	325	GDYK	KA	LLY	LC	GDD		

RESULT 18
US-10-097-340-8
; Sequence 8, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: JOHN MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: SEBASTIAN HOERSCHE
; APPLICANT: Sebastian HOERSCHE
; APPLICANT: Shubhangi KAMATKAR

Db 156 YREELKRLAKDIITSDTSGDFRNALLSLAKGDRSEDFGVNEELADSDARALYEAGERKRG 215
QY 189 TDEEKFITIFGTRSVSHLRKVDFKYMTISGFOIETIDRETSGNLEQLLLAVVKSIRSIP 248
Db 216 TDVNVFNTILTRSYFPQLRRVFQKYTKYKHDNNKVLDELKGDIEKCLTAIVKCATSKP 275
QY 249 AYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGTSGDY 308
Db 276 AFFAEKLEHQAAMKGVGTRHKALIRIMVSRSEIDMNDIKAFYQKMYGISLQAILDETKEGY 335
QY 309 KKALLLLCG 317
Db 336 EKILVALCG 344

Search completed: March 25, 2004, 08:08:25
Job time : 47 secs

ALIGNMENTS

RESULT 1
US-08-125-746-3
; Sequence 3, Application US/08125746
; Patent No. 5591633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IWASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

*COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 037227/1987
; FILING DATE: 20-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184428/1987
; FILING DATE: 23-JUL-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5591633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-125-746-3

Query Match 100.0%; Score 1600; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTL 60
Db 1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTL 60

QY 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKAGAGNEKVLTEIIASRTP 120
Db 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKAGAGNEKVLTEIIASRTP 120

QY 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQQAALF 180
Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQQAALF 180

QY 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQQAALF 180
Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQQAALF 180

QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAV 240
Db 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAV 240

QY 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
Db 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300

QY 301 KGDTSGDYKKALLLLCGEDD 320
Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 2

US-08-948-276-1
; Sequence 1, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 320
; TYPE: PRT
; ORGANISM: human
US-08-948-276-1

Query Match 100.0%; Score 1600; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTL 60
Db 1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTL 60

QY 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKAGAGNEKVLTEIIASRTP 120
Db 61 FGRDLLDDKSELTKGFKELI VALMKPSRLYDAYELKHALKAGAGNEKVLTEIIASRTP 120

QY 121 ELFAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQQAALF 180
Db 121 ELFAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQQAALF 180

QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAV 240
Db 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAV 240

QY 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
Db 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300

QY 301 KGDTSGDYKKALLLLCGEDD 320
Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 3

5225537-4
; Patent No. 5225537
; APPLICANT: POSTER, DONALD
; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
; PHOSPHOLIPID-BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,082
; FILING DATE: 29-DEC-1989
; SEQ ID NO: 4
; LENGTH: 320
5225537-4

ch 100.0%; Score 1600; DB 6; Length 320;
1 Similarity 100.0%; Pred. No. 6.4e-144; Indels 0; Gaps 0;
320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MAQVLRTGVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAAFKTL 60
1 MAQVLRTGVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAAFKTL 60
61 FGRLDLDLKSSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
61 FGRLDLDLKSSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
21 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
21 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
81 QAGELKWTGDEEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQLLAV 240
81 QAGELKWTGDEEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQLLAV 240
41 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLNFIRKFNKFNATSLYSMI 300
41 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLNFIRKFNKFNATSLYSMI 300
01 KGTSGDYKKALLLGCEDD 320
01 KGTSGDYKKALLLGCEDD 320
46-1
1. Application US/08125746
5591633
INFORMATION:
ANT: SAINO, YUSHI
ANT: IWASAKI, AKIO
ANT: SUDA, MAKOTO
OF INVENTION: ANTICOAGULANT POLYPEPTIDE
OF SEQUENCES: 5
PONDENCE ADDRESS:
ESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ESSEE: P.C.
ER: 1755 S. Jefferson Davis Highway, Suite 400
Arlington
E: Virginia
U.S.A.
22202
ER READABLE FORM:
UM TYPE: Floppy disk
UTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
WARE: Patent In Release #1.0, Version #1.25
T APPLICATION DATA:
ICATION NUMBER: US/08/125,746
NG DATE: 24-SEP-1993
SIFICATION: 530
APPLICATION DATA:
ICATION NUMBER: US 07/807,623
NG DATE: 13-DEC-1991
APPLICATION DATA:
ICATION NUMBER: JP 037227/1987
NG DATE: 20-FEB-1987
APPLICATION DATA:
ICATION NUMBER: JP 184428/1987
NG DATE: 23-JUL-1987
EY/AGENT INFORMATION:
: Oblon, No. 5591633man F.
STRATION NUMBER: 24,618
RENCE/DOCKET NUMBER: 80-074-0 DIV
MUNICATION INFORMATION:
PHONE: (703) 413-3000
FAX: (703) 413-2220

TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-125-746-1
Query Match 99.7%; Score 1595; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.9e-143;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AQVLRTGVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAAFKTLF 61
Db 1 AQVLRTGVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAAFKTLF 60
QY 62 GRDLDDLLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 121
Db 61 GRDLDDLLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 122 LRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 181
Db 121 LRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
QY 182 AGELKWTGDEEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQLLAVV 241
Db 181 AGELKWTGDEEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQLLAVV 240
QY 242 KSIRIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLNFIRKFNKFNATSLYSMIK 301
Db 241 KSIRIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLNFIRKFNKFNATSLYSMIK 300
QY 302 GDTSGDYKKALLLGCEDD 320
Db 301 GDTSGDYKKALLLGCEDD 319
RESULT 5
US-09-324-096A-2
Sequence 2, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOPW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-2
Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 5.9e-143;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQVLRTGVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAAFKTL 60
Db 8 MAQVLRTGVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAAFKTL 67
QY 61 FGRLDLDLKSSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
Db 68 FGRLDLDLKSSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
QY 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
Db 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187

181 QAGELKWTGDBEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAV 240
188 QAGELKWTGDBEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAV 247
241 VKSIRSIAPYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMI 300
248 VKSIRSIAPYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMI 307
301 KGDTSGDYKKALLLLCGEDD 320
308 KGDTSGDYKKALLLLSGEDD 327
RESULT 6
US-09-324-096A-4
; Sequence 4, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOPW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-4
Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 5,9e-143;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MAQVLRGVTVPFGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQOEISAAFKTL 60
8 MAQVLRGVTVPFGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQOEISAAFKTL 67
61 FGRDLLDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
68 FGRDLLDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
121 ELRAIKQVYEEYGSLSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALF 180
128 ELRAIKQVYEEYGSLSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALF 187
181 QAGELKWTGDBEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAV 240
188 QAGELKWTGDBEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAV 247
241 VKSIRSIAPYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMI 300
248 VKSIRSIAPYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMI 307
301 KGDTSGDYKKALLLLCGEDD 320
308 KGDTSGDYKKALLLLSGEDD 327

RESULT 7
US-09-324-096A-6
; Sequence 6, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOPW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-6
Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 5,9e-143;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MAQVLRGVTVPFGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQOEISAAFKTL 60
8 MAQVLRGVTVPFGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQOEISAAFKTL 67
61 FGRDLLDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
68 FGRDLLDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
121 ELRAIKQVYEEYGSLSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALF 180
128 ELRAIKQVYEEYGSLSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALF 187
181 QAGELKWTGDBEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAV 240
188 QAGELKWTGDBEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAV 247
241 VKSIRSIAPYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMI 300
248 VKSIRSIAPYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMI 307
301 KGDTSGDYKKALLLLCGEDD 320
308 KGDTSGDYKKALLLLSGEDD 327

RESULT 8
US-08-948-276-2
; Sequence 2, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PRT
; ORGANISM: mouse
US-08-948-276-2
Query Match 93.0%; Score 1488.5; DB 4; Length 319;
Best Local Similarity 94.0%; Pred. No. 2,5e-133;
Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

6 RGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQOEISAAFKTLFGRDL 65
4 RGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQOEISAAFKTLFGRDL 63
66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 125
64 VDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTDEKVLTEIISRTPEELSAI 123
126 KQVYEEYGSLSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALFQAGEL 185
124 KQVYEEYGSLSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALFQAGEL 183
186 KWTGDEEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAVVKSIR 245
184 KWTGDEEKFITIFGTRSVSHLRKVFQKYMVTSISGQIEETIDRETSGNLSQLLAVVKSIR 243


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Query Match      58.3%; Score 933; DB 4; Length 321;
Best Local Similarity 58.6%; Pred. No. 1.5e-80;
Matches 184; Conservative 53; Mismatches 77; Indels 0; Gaps 0;

QY 7 GTVDFPGFDERADAETLRKAMKGLGTDEESILTLTTSRNSAQRQEIISAAFKTLFGRDLL 66
DB 8 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAVNTAQRQEIIRTAKYSTIGRDLI 67
QY 67 DDLKSELGTGFEKLI VALMFKPSRLYDAYELKHALKAGTNEKVLTEIIASPTPEELRAIK 126
DB 68 DDLKSELGSGNFQVILGVMTPTLVYDQELRRAMKAGTDEGCLIEILASRTPEIRIRIS 127
QY 127 QVYEEYSGSLEDDVVGDTSGYYQRMVLVLOANRDPDAGIDEAQVEODAAALFQAGELK 186
DB 128 QTYQOQYGRSLEDDIRSDTSFMFORVLVSLAGGRDEGNLYDDALVRQDAQDLYEAGEKK 187
QY 187 WGTDEKPTITFTGTRSVHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKISRS 246
DB 188 WGTDEVKFLTVLCSSRNHLLHVFDEYKRIISQKQIEQSIKSETSGSFEDALLAIKVMCRN 247
QY 247 IPAYIAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPRKNFATSLYSMIKGTSG 306
DB 248 KSAYFAEKLKYSKMGGLGDDNTLIRVMVSRSEIDLNFIRKPRKNFATSLYSMIKGTSG 307
QY 307 DYKALLLLCGEDD 320
DB 308 DYKVLVLLCGGDD 321

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RESULT 12

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US-08-526-136-14
; Sequence 14, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319
; TYPE: amino acid

```

```

; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-526-136-14

Query Match      57.8%; Score 924; DB 3; Length 319;
Best Local Similarity 58.3%; Pred. No. 1e-79;
Matches 183; Conservative 51; Mismatches 80; Indels 0; Gaps 0;

QY 7 GTVDFPGFDERADAETLRKAMKGLGTDEESILTLTTSRNSAQRQEIISAAFKTLFGRDLL 66
DB 6 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIINVILAYRSTAQRQEIIRTAKYTTIGRDL 65
QY 67 DDLKSELGTGFEKLI VALMFKPSRLYDAYELKHALKAGTNEKVLTEIIASPTPEELRAIK 126
DB 66 DDLKSELGSGNFQVILGVMTPTLVYDQELRRAMKAGTDEGCLIEILASRTPEIRIRIN 125
QY 127 QVYEEYSGSLEDDVVGDTSGYYQRMVLVLOANRDPDAGIDEAQVEODAAALFQAGELK 186
DB 126 QTYQOQYGRSLEDDIRSDTSFMFORVLVSLAGGRDESNLYDDALMRQDAQDLYEAGEKK 185
QY 187 WGTDEKPTITFTGTRSVHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKISRS 246
DB 186 WGTDEVKFLTVLCSSRNHLLHVFDEYKRIISQKQIEQSIKSETSGSFEDALLAIKVMCRN 245
QY 247 IPAYIAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPRKNFATSLYSMIKGTSG 306
DB 246 KSAYFAEKLKYSKMGGLGDDNTLIRVMVSRSEIDLNFIRKPRKNFATSLYSMIKGTSG 305
QY 307 DYKALLLLCGEDD 320
DB 306 DYKVLVLLCGGDD 319

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RESULT 13

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US-08-526-136-2
; Sequence 2, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:

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TELEX: 200154
INFORMATION FOR SEQ ID NO: 4;
SEQUENCE CHARACTERISTICS:
LENGTH: 505
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-4

Query Match 54.7%; Score 875; DB 3; Length 503;
Best Local Similarity 55.2%; Pred. No. 9e-75;
Matches 174; Conservative 58; Mismatches 83; Indels 0; Gaps 0;

6 RGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEIISAAFKTLFGKDL 65
191 RGTITDASGDFPLRDAEVLKAMKGFQDEQAIDCLGSRNKQKQIILLFKTAYGKDL 250
66 LDDLKSELTGKPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
251 IKDLKSELNGFNFKETILALMKTPVLFDAYEIKAEIKAGTDEACLIBELASRSNEHIREL 310
126 KQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAALFOAGEL 185
311 NRVTKEFKTKLEAIRSDTSGHFQRLIISLQGNRDESTNVDMLVQRDVQELYAAGEN 370
186 KWTDEKFIITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLLAVVKSIR 245
371 RLGTDESKFNAILCSRAHLVAVFNEYQRTGRIEKSICREMSGDLQGLAVVCKL 430
246 SIPAYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKPKNFATSLYSMIKGDT 305
431 NTPAFFAERLNKAMRGAGTKDRTLIRWVSSEIDLLDIRAEYKRLYKSLYHDITGDT 490
306 GDYKALLLCGEDD 320
491 GDYRKILLKICGND 505

RESULT 15
US-08-948-276-5
Sequence 5, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 323
TYPE: PRT
ORGANISM: human
US-08-948-276-5

Query Match 50.7%; Score 811; DB 4; Length 323;
Best Local Similarity 50.2%; Pred. No. 5.7e-69;
Matches 158; Conservative 61; Mismatches 96; Indels 0; Gaps 0;

6 RGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEIISAAFKTLFGKDL 65
9 RGTVDYDPDFSPSDAEAIQKAIIRGIGTDERKMLISILTSRNSAQRQLIVKEYQAAYGKEL 68
66 LDDLKSELTGKPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
69 KDDLKGLDLSGHEHLMVALVTPVAFDAKQLKSKMGAGTNEDEALIEIITRTSRQMKDI 128
126 KQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAALFOAGEL 185
129 SQAYVTVYKKSIGDDISSETSGDFKALLTLADGRDESLKVEHLAKQDAQILYKAGEN 188
186 KWTDEKFIITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLLAVVKSIR 245

SEQUENCE CHARACTERISTICS:
LENGTH: 503
E: amino acid
OLOGY: N/A
136-2

54.7%; Score 875; DB 3; Length 503;
55.2%; Pred. No. 9e-75;
Conservative 58; Mismatches 83; Indels 0; Gaps 0;

6 RGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEIISAAFKTLFGKDL 65
189 RGTITDASGDFPLRDAEVLKAMKGFQDEQAIDCLGSRNKQKQIILLFKTAYGKDL 248
66 LDDLKSELTGKPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
249 IKDLKSELNGFNFKETILALMKTPVLFDAYEIKAEIKAGTDEACLIBELASRSNEHIREL 308
126 KQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAALFOAGEL 185
09 NRVTKEFKTKLEAIRSDTSGHFQRLIISLQGNRDESTNVDMLVQRDVQELYAAGEN 368
186 KWTDEKFIITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLLAVVKSIR 245
369 RLGTDESKFNAILCSRAHLVAVFNEYQRTGRIEKSICREMSGDLQGLAVVCKL 428
246 SIPAYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKPKNFATSLYSMIKGDT 305
29 NTPAFFAERLNKAMRGAGTKDRTLIRWVSSEIDLLDIRAEYKRLYKSLYHDITGDT 488
06 GDYKALLLCGEDD 320
89 GDYRKILLKICGND 503

36-4
4, Application US/08526136
6107089
INFORMATION:
ANT: Towle, Christine A. et al.
OF INVENTION: ANNEXIN XI
OF SEQUENCES: 36
PONDENCE ADDRESS:
ESSEE: Fish & Richardson
ET: 225 Franklin Street
Boston
E: Massachusetts
TRY: U.S.A.
02110-2804
ER READABLE FORM:
UM TYPE: 3.5" Diskette, 1.44 Mb
UTER: IBM PS/2 Model 50Z or 55SX
ATING SYSTEM: IBM P.C. DOS (Version 3.30)
WARE: Wordperfect (Version 5.0)
T APPLICATION DATA:
NG DATE: US/08/526,136
SIFICATION: 435
APPLICATION DATA:
ICATION NUMBER: US/08/214,036
NG DATE:
ICATION NUMBER: 07/837,775
NG DATE: February 13, 1992
ICATION NUMBER: 07/764,465
NG DATE: September 23, 1991
Y/AGENT INFORMATION:
Clark, Paul T.
SITATION NUMBER: 30,162
RENCE/DOCKET NUMBER: 00786/099001
MUNICATION INFORMATION:
PHONE: (617) 542-5070
FAX: (617) 542-8906

Db 189 RWGTDEKFTTILCLRSPPQLKLTDFEYRNISQKDIVDSIKGELSGHPEDLLLAIVNCR 248
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSIMIKGDT 305
Db 249 NTPAFLAERHLAKGIGTDEFTLNRINVSRSSEIDLDIRTEFKKHGYSLYSIAKSDTS 308
Qy 306 GDYKALLLGGEDD 320
Db 309 GDYEITLLKICGDD 323

RESULT 16
US-08-526-136-13
; Sequence 13, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-526-136-13

Query Match 48.8%; Score 780; DB 3; Length 466;
Best Local Similarity 48.1%; Pred. No. 8.5e-66;
Matches 153; Conservative 66; Mismatches 99; Indels 0; Gaps 0;
Qy 1 MAQVLRTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAFKTL 60
Db 149 VTQVTQGTIRPAANFADIRDAEILRKAMKGFDTDEQAIVDVVANRSDQRKIAAFKTS 208
Qy 61 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 120
Db 209 YGKDLKDLKSELSENMEELILALFMPPTYYDAWSLRKAMQAGTQERVLIELCTRTNQ 269
Qy 121 ELRAIKQVYEEYSGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODAQLF 180
Db 269 EIREIVCYQSEFGDRLEKDIRSDTSGHFERLLVSMCGNRDENQNSINHQAQEDAQLY 328

Qy 181 QAGELKMGTDDEKFTITFTGTRSVSHLRKVPDKWMTYISGFOIETIDRETSGNLQOLLAV 240
Db 329 QAGELGTDDESCFNMLATRSPPQLRATMEAYSRMANRDLSSVSREFSGYVESGLKTI 388
Qy 241 VKSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
Db 389 LQCALNRPAFAERLYYAMKAGTDDSTLVIRIVVTRSEIDLVIQKQFAQMYQKTLGTMI 448
Qy 301 KGDTSGDYKALLLCCG 318
Db 449 AGDTSGDYRRLLLAIVGQ 466

RESULT 17
US-08-948-276-6
; Sequence 6, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: human
US-08-948-276-6

Query Match 40.8%; Score 653; DB 4; Length 346;
Best Local Similarity 44.3%; Pred. No. 6.4e-54;
Matches 137; Conservative 59; Mismatches 113; Indels 0; Gaps 0;
Qy 9 VTDFPFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAFKTLFGDRLLDD 68
Db 36 VSPYTFNFPSSDVAALHKAIMVKGVDATIIDILTKRNNAQOIKAAVLOETGKPLDET 95
Qy 69 LKSELTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPELRAIKOV 128
Db 96 LKCAULTGHLEEVVLLAKTPAQFADALRAAMKGLGTDEDTLTIILASRTEKNEIRDINRV 155
Qy 129 YEEYVGSLSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODAQLFOAGELKMG 188
Db 156 YREELKRDIAKIDTSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKG 215
Qy 189 TDEEKFTITFTGTRSVSHLRKVPDKWMTYISGFOIETIDRETSGNLQOLLAVVKSIRSP 248
Db 216 TDVNVENTILTRSPQLRRVFKYTKYKSHDMKNVLDLELKGDIKCLTAIVKCATSKP 275
Qy 249 AYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSIMIKGDTSGDY 308
Db 276 AFPAEKLHQAAMKGVGTRHKAIRIMVSRSEIDMNDIKAFYQKMYGISLQCAILDETQGY 335
Qy 309 KKALLLLCG 317
Db 336 EKLLVALCG 344

RESULT 18
US-09-919-172-39
; Sequence 39, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469

ILLING DATE: 2000-07-28
SEQ ID NOS: 102
PERL Program
39
346
PRT

SM: Homo sapiens

Y: misc feature

INFORMATION: Incyte ID No. 6673545 1303785CD1

172-39

ch 40.6%; Score 649; DB 4; Length 346;
al Similarity 44.0%; Pred. No. 1.5e-53;
136; Conservative 60; Mismatches 113; Indels 0; Gaps 0;
9 VTDPPGDERADAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRLDD 68
36 VSPYTPNPSSDVAALHKAIMVKGVDEATIIDLTKNNAAQROQIKAAYLQETGKPLDET 95
69 LKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKOV 128
96 LKALTGHEVVLALLKTPAQFADDELRAAMKGLGTDEDTLIELASRTNKEIRDINRV 155
229 YEEYEGSSLEDDVVDGTSYQYRMVLLQANRPDPAGIDEAQVEQDAQALFOAGELKWG 188
56 YREELKEDLAKDITSDSGDFRNALLSLAKGRSEDFGVNEDLADSDARALYEAGERRKG 215
89 TDEKEFTITFTRSVSHLRKVKFDKYMVTISGFOIETDRETSNLEQLLAVVKSIRSIP 248
16 TDVNVFNTLTRYPQLRRVFOKYTKYKDHMMKVLDLELKGDIKELCTAIVKCATSKP 275
49 AYLAETLYAMKAGTDDHTLIRVWVSERSEIDLFRNIRKEFRKPNFATSLYSMIKGTSGDY 308
76 AFFAEKLHQAAMKGVGTRHKAIRIMVSRSEIDMDMDIKAFYQKMYGSLCQAILDETKEY 335
09 KXALLLCG 317
36 EKILVALCG 344

47B-16

16. Application US/09010147B

6653445

INFORMATION:

PLICANT: Ni et al.

FILE OF INVENTION: Human Proteins

MBER OF SEQUENCES: 24

RESPONSE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

PUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

URRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010.147B

FILING DATE: 12-Jan-1997

CLASSIFICATION: <Unknown>

IOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034.205

FILING DATE: 21-Jan-1997

APPLICATION NUMBER: US 60/034.204

FILING DATE: 21-Jan-1997

TORNEY/AGENT INFORMATION:

NAME: Jonathan L. Klein

REGISTRATION NUMBER: 41,119.
REFERENCE/DOCKET NUMBER: PF353

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 324 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-010-147B-16

Query Match 37.0%; Score 591.5; DB 4; Length 324;
Best Local Similarity 38.1%; Pred. No. 4e-48;
Matches 120; Conservative 76; Mismatches 118; Indels 1; Gaps 1;
QY 5 LRCVTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRD 64
Db 7 VQGTITPAPNPNFIMDAQMLGGALQGFDCDKDMLINILTORCNAQRMMAEAYQSMYGRD 66
QY 65 LDDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
Db 67 LIGDLREQUSDHPKDVNAGLMYPPLDYDAHELWHAMKGVGTDCNCLIEILASRTNGEIFQ 126
QY 125 IKOWYEEYEGSSLEDDVVDGTSYQYRMVLLQANRPDPAGIDEAQVEQDAQALFOAGE 184
Db 127 MRAYCLOYSNNLOEDIIYSETSGHFRDTLMNLVQGTRE-EGYTDPAQAQDAMVLWEACQ 185
QY 185 LKNGTDEEKPITITFTRSVSHLRKVKFDKYMVTISGFOIETDRETSNLEQLLAVVKS 244
Db 186 QKTGEHKTMLQMLCNKSYQQLRLVFQEPONISGQDMVDALNECYDGYFQELLVAIVLCV 245
QY 245 RSPAYLAETLYAMKAGTDDHTLIRVWVSERSEIDLFRNIRKEFRKPNFATSLYSMIK 304
Db 246 RDKPAYFAVRLYSAIHDFGFHNTVIRILITARGEIDLLTIRKRYKERYGKSLFHDINFA 305
QY 305 SGDYKKALLLCGED 319
Db 306 SGHYKALLAICAGD 320

RESULT 20

US-09-325-932A-62

Sequence 62, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of forestry plant develo

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 62

LENGTH: 316

TYPE: PRT

ORGANISM: Pinus radiata

US-09-325-932A-62

Query Match 23.7%; Score 378.5; DB 4; Length 316;
Best Local Similarity 32.1%; Pred. No. 6.6e-28;
Matches 96; Conservative 58; Mismatches 142; Indels 3; Gaps 2;

QY 20 DAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRLDDDLKSELTKGFEK 79

Db 16 DCEQLRTAFAGWTNEKLIISILGHNAQQRKLIQRTYAETYGEDLLKALDRLTNDFR 75

QY 80 LIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEYEGSSLED 139

Db 76 LVVLSLDPADRDAYLANEATKRWTSNOVLMETACTSPQOLLMARQAYHARYKSMEE 135
Qy 140 DVVGTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFQ-AGELKMGTDSEKFTIF 198
Db 136 DVAHTTGDPRKLLVPLGSSYRNDGDEVNMTLAKAEAKILHEKISEKAYG--HEDLIRIL 193
Qy 199 GTRSVSHURKVPDKYMTISGQIETIDRETSNLEQLLLAVVKSIRSIPAYLAETLYA 258
Db 194 ATRSKAQVNATNLNHYKNEFGNDINKDLTKDPKDAFLATILRATVKCLTRPEKYFEKVLRLA 253
Qy 259 MKGAGTDHTLIRVMVSRSEIDLNFIRKFKVPATSLYSIMKGTSGDYKKALLLGG 317
Db 254 INKRGTDGALTRVVATRAEDVMKFISEYQRRNSIPLDRAIVKDTTGDYKMLLALIG 312

RESULT 21

US-09-621-976-4980
; Sequence 4980, Application US/09621976
; Patent No. 6639063

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4980
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-621-976-4980

Query Match 16.3%; Score 261; DB 4; Length 151;
Best Local Similarity 38.4%; Pred. No. 3.3e-17;
Matches 56; Conservative 29; Mismatches 61; Indels 0; Gaps 0;

Qy 174 ODAQALFOAGELKWTGDEKFTITIGTSVSHLRKVPDKYMTISGQIETIDRETSNGL 233
Db 4 QDAMVLEACQKQTEGHEKMLQMLCNKSYQQLRLVFEQFQISQDWDVDAINECYDGYF 63
Qy 234 EQLLAVVKSIRSIPAYLAETLYAMKAGAGTDHDLIRVMVSRSEIDLNFIRKFKRKNFA 293
Db 64 QELLVAIVLCVDKPAYFAYRLYSALHDFGFHNTKTVIRILIRSEIDLTLTKRYKRYG 123
Qy 294 TSLYSIMIKGTSGDYKKALLLGGED 319
Db 124 KSLFHDIRNFASGHYKKALLAICAGD 149

RESULT 22

US-09-325-932A-65
; Sequence 65, Application US/09325932A
; Patent No. 6451604

GENERAL INFORMATION:

; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develo
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 65

LENGTH: 239

TYPE: PRT

ORGANISM: Pinus radiata

US-09-325-932A-65

Query Match 15.3%; Score 245.5; DB 4; Length 239;

Best Local Similarity 28.9%; Pred. No. 1.9e-15;
Matches 65; Conservative 113; Mismatches 113; Indels 1; Gaps 1;

Qy 20 DAETLRKAMKGLGTDEESILTLTSRNAQOEISAAFKTLFGRDLDLDDKSELTKGPEK 79
Db 16 DAEQLQKAFAGWGTNEDLIISILPHRNAQKVIQRYAETYGEDLLKALDKELSSDPER 75
Qy 80 LIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEYGGSSLED 139
Db 76 SVLLWTLDPADRDPAERDAFLSNEATKRLTSSNWVLMETACTRSSMELPMVQAYHARYKKSLEE 135
Qy 140 DVVGTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFQAGELKMGTDSEKFTIFG 199
Db 136 DIAVHTTGDPRKLLVPLASTFRYEGPEVNMVTLARSEAKILHEKIHKEK-AYNHDELIRIVT 194
Qy 200 TRSVSHLRKVPDKYMTISGQIETIDRETSNLEQLLLAVVKS 244
Db 195 TRSKAQVNATNLNHYKNEFGNDINKDLKADPNDFELKLLRSIAIKCL 239

RESULT 23

US-09-325-932A-66
; Sequence 66, Application US/09325932A
; Patent No. 6451604

GENERAL INFORMATION:

; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develo
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Pinus radiata

US-09-325-932A-66

Query Match 14.5%; Score 232; DB 4; Length 184;
Best Local Similarity 35.0%; Pred. No. 2.5e-14;
Matches 57; Conservative 33; Mismatches 73; Indels 0; Gaps 0;

Qy 20 DAETLRKAMKGLGTDEESILTLTSRNAQOEISAAFKTLFGRDLDLDDKSELTKGPEK 79
Db 16 DSELRKAFAGWGTNEDLIISILPHRNAQKVIQRYAETYGEDLLKALDKELSSDPER 75
Qy 80 LIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEYGGSSLED 139
Db 76 AVFLWTLDPADRDPAERDAVISHGAIKKNVNAKISLLEISSAFSSAELLMVQAYHARYKKSLEE 135
Qy 140 DVVGTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFQA 182
Db 136 DVVAHTSGNFRKLLVALVSVSYRYEGPEVDMHLASVEAKKUSE 178

RESULT 24

US-09-157-257-4
; Sequence 4, Application US/09157257
; Patent No. 6375954

GENERAL INFORMATION:

; APPLICANT: Dutta, Sukanta K.
; APPLICANT: Biswas, Biswajit
; APPLICANT: VENULAPALLI, Ramesh
; TITLE OF INVENTION: A SIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR
; TITLE OF INVENTION: POTOMAC HORSE FEVER
; FILE REFERENCE: 8172-9016
; CURRENT APPLICATION NUMBER: US/09/157,257
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 60/059,252
; EARLIER FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 48

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- protein search, using sw model

March 25, 2004, 08:00:30 ; Search time 45 Seconds
(without alignments)
2243.685 Million cell updates/sec

US-09-787-923-2
1600
1 MAQVLGVTDFPGFDERAD.....KGDTSYKALLLCGEDD 320

le: BLOSUM62
Gapop 10.0 ; Gapext 0.5
1017041 seqs, 315518202 residues

r of hits satisfying chosen parameters: 1017041

seq length: 0
seq length: 2000000000
sing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

No. is the number of results predicted by chance to have a
greater than or equal to the score of the result being printed,
s derived by analysis of the total score distribution.

SUMMARIES

ore	Query Match	Length	DB	ID	Description
595	99.7	320	4	Q8WV69	Q8WV69 homo sapien
4.5	92.8	319	11	Q99LA1	Q70371 rattus norv
390	86.9	302	11	Q70371	Q78219 xenopus lae
255	78.4	318	13	Q7SZ19	Q7zy99 xenopus lae
255	78.4	351	13	Q7ZV99	Q73445 oryzias lat
052	65.8	317	13	Q93445	Q803A1 brachydania
027	64.2	317	13	Q803A1	Q804G6 brachydania
025	64.1	317	13	Q804G6	Q8C6X0 mus musculus
942	58.9	476	11	Q8CEX0	Q991X6 mus musculus
942	58.9	667	11	Q991X6	Q8B6S4 mus musculus
940	58.8	673	11	Q8BSS4	Q7tmn7 mus musculus
925	57.8	319	11	Q7TMN7	Q7t391 brachydania
915	57.2	483	13	Q7T391	Q804G4 brachydania
876	54.8	320	13	Q93444	Q93444 oryzias lat
866	54.1	508	13	Q93447	Q93447 oryzias lat

17	862	53.9	485	13	Q804G3	Q804g3 brachydania
18	859	53.7	321	13	Q90X16	Q90x16 xenopus lae
19	857	53.6	503	11	Q921F1	Q921f1 mus musculus
20	855	53.4	321	13	Q804G7	Q804g7 brachydania
21	841.5	52.6	327	11	Q8K2N9	Q8k2n9 mus musculus
22	837.5	52.3	327	6	Q95L54	Q95l54 bos taurus
23	823.5	51.5	327	6	O97529	O97529 oryctolagus
24	809	50.6	323	11	Q8C1X9	Q8c1x9 mus musculus
25	774	48.4	463	11	Q922A2	Q922a2 mus musculus
26	771	48.2	463	11	Q8VIN2	Q8vin2 rattus norv
27	770	48.1	463	11	Q8BP75	Q8bp75 mus musculus
28	753	47.1	324	5	Q81GJ8	Q81g18 drosophila
29	752	47.0	324	5	Q9NL61	Q9nl61 bombyx mori
30	744.5	46.5	301	11	Q921D0	Q921d0 mus musculus
31	725	45.3	323	5	Q9NL59	Q9nl59 bombyx mori
32	719	44.9	324	5	Q9NG55	Q9ng55 drosophila
33	716	44.8	321	5	Q8WPG9	Q8wpg9 bombyx mori
34	715	44.7	486	5	Q8WPH0	Q8wph0 bombyx mori
35	711	44.4	323	5	Q9NGG6	Q9ngg6 bombyx mori
36	707	44.2	323	5	Q9NL60	Q9nl60 bombyx mori
37	706	44.1	497	5	Q27512	Q27512 caenorhabdi
38	704.5	44.0	339	4	Q8TBV2	Q8tbv2 homo sapien
39	703	43.9	338	13	Q7SZ98	Q7sz98 xenopus lae
40	700	43.8	324	5	Q969D3	Q969d3 drosophila
41	696.5	43.5	339	11	Q9CZ17	Q9czi7 mus musculus
42	688.5	43.0	340	13	Q7ZXM2	Q7zxm2 xenopus lae
43	685	42.8	315	5	Q95V57	Q95v57 artemia san
44	680	42.5	317	11	Q99JG3	Q99jg3 mus musculus
45	677	42.3	340	13	Q7T3A8	Q7t3a8 brachydania
46	676	42.2	340	13	Q804H2	Q804h2 brachydania
47	673	42.1	357	6	Q8WJBS	Q8wjbs oryctolagus
48	667	41.7	337	13	Q93446	Q93446 oryzias lat
49	664.5	41.5	330	5	Q86DV3	Q86dv3 schistosoma
50	663	41.4	341	13	Q804H0	Q804h0 brachydania
51	658.5	41.2	343	13	Q7SZ11	Q7sz11 xenopus lae
52	656	41.0	322	5	Q9VXG4	Q9vxg4 drosophila
53	656	41.0	511	5	Q9VXG3	Q9vxg3 drosophila
54	653	40.8	346	6	Q8HZM6	Q8hzm6 equus cabal
55	646	40.4	316	13	Q98SH7	Q98sh7 brachydania
56	635.5	39.7	314	13	Q92128	Q92128 xenopus lae
57	630.5	39.4	337	13	Q804G9	Q804g9 brachydania
58	620	38.8	342	13	Q804H1	Q804h1 brachydania
59	617	38.6	337	13	Q804G8	Q804g8 brachydania
60	609	38.1	290	13	Q804G2	Q804g2 brachydania
61	581.5	36.3	322	5	Q27864	Q27864 caenorhabdi
62	573.5	35.8	415	11	Q8CCV9	Q8ccv9 mus musculus
63	572	35.8	209	11	Q8BSL2	Q8bsl2 mus musculus
64	558.5	34.9	337	13	Q7ZWX0	Q7zwx0 xenopus lae
65	540	33.8	317	5	Q27473	Q27473 caenorhabdi
66	530	33.1	345	4	Q9HBJ6	Q9hbj6 homo sapien
67	528.5	33.0	222	11	Q99KH3	Q99kh3 mus musculus
68	528	33.0	365	5	Q9XY89	Q9xy89 schistosoma
69	524.5	32.8	180	13	O57570	O57570 brachydania
70	520	32.5	345	11	Q9CQS1	Q9cqs1 mus musculus
71	515.5	32.2	347	5	Q9XZL9	Q9xz19 taenia soli
72	511	31.9	316	10	Q9C9X3	Q9c9x3 arabidopsis
73	509.5	31.8	331	5	Q9BI01	Q9bi01 globodera p
74	508.5	31.8	304	11	Q9D272	Q9d272 mus musculus
75	508.5	31.8	346	5	Q9NGU7	Q9ngu7 taenia soli
76	507	31.7	316	10	Q9C5V4	Q9c5v4 arabidopsis
77	504	31.5	276	4	Q96H89	Q96h89 homo sapien
78	491.5	30.7	321	10	Q84Q48	Q84q48 oryza sativ
79	489	30.6	196	11	Q9R0V2	Q9r0v2 mus musculus
80	472.5	29.5	333	10	Q9ZR53	Q9zr53 medicago sa
81	458.5	28.7	341	5	Q8ITJ0	Q8itj0 heterodera
82	451.5	28.2	316	10	Q9ZR07	Q9zru7 capsicum an
83	448	28.0	334	10	Q9FUG5	Q9fug5 ceratopter
84	435.5	27.2	316	10	Q9XEN8	Q9xen8 nicotiana t
85	427	26.7	330	10	Q9FUG6	Q9fug6 ceratopter
86	426.5	26.7	256	13	Q8AVS3	Q8av83 xenopus lae
87	423	26.4	313	10	O65848	O65848 medicago tr
88	414	25.9	315	10	P93158	P93158 gossypium h
89	406.5	25.4	472	3	O59907	O59907 neurospora

90 405.5 25.3 321 10 Q9ZVJ7 arabidopsis
 91 404 25.2 315 10 O81535 lycopersico
 92 402.5 25.2 308 10 Q42922 medicago sa
 93 400.5 25.0 321 10 Q9SE45 arabidopsis
 94 397.5 24.8 314 10 Q24132 nicotiana t
 95 391.5 24.5 318 10 Q9CSV3 arabidopsis
 96 391 24.4 317 10 Q96527 arabidopsis
 97 390.5 24.4 318 10 Q9LX08 arabidopsis
 98 390 24.4 317 10 Q9SY70 arabidopsis
 99 389.5 24.3 314 10 Q24131 nicotiana t
 100 386.5 24.2 314 10 O81536 lycopersico

ALIGNMENTS

RESULT 1
 Q8WV69 PRELIMINARY; PRT; 320 AA.
 AC Q8WV69;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Annexin A5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
 CC -!- CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
 DR EMBL; BC018671; AAH18671.1; -.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
 KW Repeat.
 SQ SEQUENCE 320 AA; 35924 MW; 45FAC411DDBA4D1A CRC64;

Query Match 99.7%; Score 1595; DB 4; Length 320;
 Best Local Similarity 99.7%; Pred. No. 4.8e-107;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAQVLRTGVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSRNAQRQEISAAFKTL 60
 DB 1 MAQVLRTGVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSRNAQRQEISAAFKTL 60
 QY 61 FGRLDLDLKSLLTKGFEKLIIVALKMPSRLYDAYELKHALKGAGNEKVLTEIISRTPE 120
 DB 61 FGRLDLDLKSLLTKGFEKLIIVALKMPSRLYDAYELKHALKGAGNEKVLTEIISRTPE 120
 QY 121 ELRAIKQVVEEYGSLSDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVVEEYGSLSDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
 QY 181 QAGELKWTGDEKFTITIFGTRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAV 240
 DB 181 QAGELKWTGDEKFTITIFGTRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAV 240
 QY 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKNFATSLYMSI 300
 DB 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKNFATSLYMSI 300

QY 301 KGDTSGDYKKALLLCCGEDD 320
 DB 301 KGDTSGDYKKALLLCCGEDD 320
 RESULT 2
 Q99LA1 PRELIMINARY; PRT; 319 AA.
 AC Q99LA1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Annexin A5.
 GN ANXA5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
 CC -!- CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
 DR EMBL; BC003716; AAH03716.1; -.
 DR HSSP; P14668; 1A8B.
 DR MGD; MGI:106008; Anxa5.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
 KW Repeat.
 SQ SEQUENCE 319 AA; 35738 MW; 52E2C7CCEA386917 CRC64;

Query Match 92.8%; Score 1484.5; DB 11; Length 319;
 Best Local Similarity 93.7%; Pred. No. 4.5e-99;
 Matches 296; Conservative 9; Mismatches 10; Indels 1; Gaps 1;
 QY 6 RGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSRNAQRQEISAAFKTLFGRLD 65
 DB 4 RGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSRNAQRQEISAAFKTLFGRLD 63
 QY 66 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGNEKVLTEIISRTPEELRAI 125
 DB 64 VDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIISRTPEELSAI 123
 QY 126 KQVVEEYGSLSDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 185
 DB 124 KQVVEEYGSLSDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 183
 QY 186 KWTGDEKFTITIFGTRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAVKVSIR 245
 DB 184 KWTGDEKFTITIFGTRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAVKVSIR 243
 QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKNFATSLYMSIKGDT 305
 DB 244 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKNFATSLYMSIKGDT 303
 QY 306 GDYKALLLCC-GEDD 320
 DB 304 GDYKALLLCCGEDD 319
 RESULT 3
 O70371

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PRELIMINARY;                                PRT;   302 AA.

19998 (TrEMBLrel; 07, Created)
19998 (TrEMBLrel; 07, Last sequence update)
00003 (TrEMBLrel; 25, Last annotation update)
in V (Fragment).
Chorogryles (Rat).
a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
KID=101116;

3 FROM N.A.

lung;
Edelman J.L., Kang T., Sachs G.;
tinal V may function as a signaling protein for vascular
tial growth factor receptor-2/Flk-1.";
. Biophys. Res. Commun. 258:713-721(1999).
A PAIR OF ANNEKIN REPEATS MAY FORM ONE BINDING SITE FOR
ANNEKIN AND PHOSPHOLIPID (BY SIMILARITY).
ILARITY: BELONGS TO THE ANNEKIN FAMILY.
ILARITY: CONTAINS 4 ANNEKIN REPEATS.
0051895; AAC06290.1; -.
44668; LA8B.
0005509; F:calcium ion binding; IEA.
0005544; F:calcium-dependent phospholipid binding; IEA.
; IP001464; Annekin.
000191; annekin; 4.
P000196; ANNEKIN.
PD000143; Annekin; 4.
BM000335; ANK; 4.
PS00223; ANNEKIN; 3.
; Calcium; Calcium-binding; Calcium/phospholipid-binding;
302 302
3 302 AA; 33965 MW; AB9FB40934A3D007 CRC64;
86.9%; Score 1390; DB 11; Length 302;
Similarity 92.0%; Pred. No. 2.7e-92;
6; Conservative 12; Mismatches 12; Indels 0; Gaps 0

6 LGRTVTDPGPGERADAETLRKAMKGLGTDDESILTLTSRNAORQISIAFKTLFGD 64
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
6 LGRTVDFSGFGRADAELVLRKAMKGLGTDDESIILNLTARSAORQIATSEFKTLFGD 62
LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTEKVLTIIASRTPEELRA 124
LVNDMKSELTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTDEKVLTIIASRTPEELRA 122
IKQVVEEYGSLEDDVGDTSGYQRMVLVLQANRPDAGIDBAQVQDAQALFQAGE 184
IKQVVEEYGSLEDDVGDTSGYQRMVLVLQANRPDPTAIDDAQVELDAQALFQAGE 182
LKWGTDDEEKFIITGTRSVSHLRKVFDKWTMTISGQIETIDRETSGNLEQLLAVKSI 244
LKWGTDDEEKFIITGTRSVSHLRVFDKWTMTISGQIETIDRETSGNLEQLLAVKSI 242
RSIPAYLAETLYAMKAGCTDDHTLIRVWVSSEIDLNFNRKFNKFNATSLYSMIKGD 304
RSIPAYLAETLYAMKAGCTDDHTLIRVVSSEIDLNFNRKFNKFNATSLYSMIKGD 302

PRELIMINARY;                                PRT;   318 AA.

0003 (TrEMBLrel; 25, Created)
0003 (TrEMBLrel; 25, Last sequence update)
00003 (TrEMBLrel; 25, Last annotation update)
ical protein (Fragment).
laevis (African clawed frog).
a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Batrachia; Anura; Mesobatrachia; Pipoides; Pipidae;

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RESULT 5
Q7ZY99 PRELIMINARY; PRT; 351 AA.
AC Q7ZY99;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043882; AAH43882.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR Hypothetical protein.
KW NON_TER
FT
SQ SEQUENCE 351 AA; 39321 MW; FF71B665A38CA8AE CRC64;

Query Match 78.4%; Score 1255; DB 13; Length 351;
Best Local Similarity 75.6%; Pred. No. 1.8e-82;
Matches 238; Conservative 44; Mismatches 33; Indels 0; Gaps 0;

QY 6 RGTVDFFGPFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEIISAFAKTLFGKDL 65
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 36 RGTIDFFGFKANDAEALRKAMKGLGTDEEAIKILISRNAQRQEIIDVAYKTLFGKDL 95
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 LDDLKSELTGKFKELIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 96 VDDLKSEISGKENLIVALTMPALYDAYELFHAMKAGATTENVLTELASRTTDEVRHI 155
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 126 KQVYEEVSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 156 KQVYQEQYELEDSTGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 215
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 186 KWTGDEEKFTITFGTRSVSHLRKVFQKMTISGFOIETIDRETSGNLEQLLAVVKSR 245
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 216 KWTGDEEKFTITFGTRSVSHLRKVFQKMTISGFOIETIDRETSGNLEQLLAVVKSR 275
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 SIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLNFIRKFRKNFATSLYSMIKGDTS 305
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 276 SIPEYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLNFIRKFRKNFATSLYSMIKGDTS 335
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 306 GDYKALLLLCGEDD 320
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 336 GDYRNALLLLCGEDD 350
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q93445 PRELIMINARY; PRT; 317 AA.
ID Q93445
AC Q93445;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin max2.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

RESULT 7
Q803A1 PRELIMINARY; PRT; 317 AA.
ID Q803A1
AC Q803A1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

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BC046873; AAH46873.1; F:calcium ion binding; IEA.
:0005509; F:calcium-dependent phospholipid binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
IPR001464; Annexin.
PF00191; annexin; 4.
; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
SMO0335; ANX; 4.
TE; PS00223; ANNEXIN; 4.
etic acid protein.
NCE 317 AA; 35060 MW; B33DA22F3DFBBD5 CRC64;
ch 64.2%; Score 1027; DB 13; Length 317;
al Similarity 64.4%; Pred. No. 4.5e-66;
203; Conservative 49; Mismatches 61; Indels 2; Gaps 1;
6 RGTVPDPPGDERADATLRKAMKGLGTDEESILTILTSRSNAQOEISAAFKTLFGDRL 65
4 RGTVPQSGFNANSDAEVLKAMKGLGTDEESILTILTSRSNAQOEISAAFKTLHGKDL 63
66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
64 VNDLKSELGGKFEDLIVALTMTPTIIEVTCLRNAIKAGTDEKVLIEILASRSPNEVNEI 123
126 KQVVEEYSGSLEDVVGDTSGYYQYRMVLLQANRPDPADAGIDEAQVEQDAQALFQAGEL 185
124 KSSYKREHDKDLEEDVTGDTGGHFERMLAVLLQASR--QQIQESLIQSDAQALFAAGEQ 181
186 KWTGDEBEKFTITFGRSVSHLRKVFQKYMITSQFQIBETIDRETSGNLEQLLLAVVKSIR 245
182 KYGTDEGQFITILGNRSNAHLRVRFEYRKLSGFEIEESIQRETSGSLQEILLAVVKAR 241
246 SIPAYLAETLYYAMKGAGTDHLLIRVWMSRSEIDLNIKRFKRNKFNATSLYSIMIKGDT 305
42 SVPGYFADSLYAAAMKGAGTDQTLIRIMVTRSEVLLDIRAEFRKFRATSLHKMIQSDTS 301
06 GDYKALLLCCGDD 320
02 GDYKRTLLLLCGGDD 316
PRELIMINARY; PRT; 317 AA.
-2003 (TrEMBLrel. 24, Created)
-2003 (TrEMBLrel. 24, Last sequence update)
-2003 (TrEMBLrel. 25, Last annotation update)
n 5.
danio rerio (zebrafish) (Danio rerio).
ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
pterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
idae; Danio.
axID=7955;
CE FROM N.A.
S.A.; Olson E.S.; Halpern M.E.;
ebrafish Annexin (Gene Family);
Res. 0:0-0(2003).
AY178799; AAC02073.1; --
:0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
ro; IPR001464; Annexin.
PF00191; annexin; 4.
; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
SMO0335; ANX; 4;
E; PS00223; ANNEXIN; 4.
ICE 317 AA; 35057 MW; 082CF83C9F29D6AF CRC64;
ch 64.18; Score 1025; DB 13; Length 317;
1 Similarity 64.4%; Pred. No. 6.2e-66;
203; Conservative 49; Mismatches 61; Indels 2; Gaps 1;

QY 6 RGTVPDPPGDERADATLRKAMKGLGTDEESILTILTSRSNAQOEISAAFKTLFGDRL 65
Db 4 RGTVPQSGFNANSDAEVLKAMKGLGTDEESILTILTSRSNAQOEISAAFKTLHGKDL 63
QY 66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db 64 VNDLKSELGGKFEDLIVALTMTPTIIEVTCLRNAIKAGTDEKVLIEILASRSPNEVNEI 123
QY 126 KQVVEEYSGSLEDVVGDTSGYYQYRMVLLQANRPDPADAGIDEAQVEQDAQALFQAGEL 185
Db 124 KSSYKREHDKDLEEDVTGDTGGHFERMLAVLLQASR--QQIQESLIQSDAQALFAAGEQ 181
QY 186 KWTGDEBEKFTITFGRSVSHLRKVFQKYMITSQFQIBETIDRETSGNLEQLLLAVVKSIR 245
Db 182 KYGTDEGQFITILGNRSNAHLRVRFEYRKLSGFEIEESIQRETSGSLQEILLAVVKAR 241
QY 246 SIPAYLAETLYYAMKGAGTDHLLIRVWMSRSEIDLNIKRFKRNKFNATSLYSIMIKGDT 305
Db 42 SVPGYFADSLYAAAMKGAGTDQTLIRIMVTRSEVLLDIRAEFRKFRATSLHKMIQSDTS 301
QY 06 GDYKALLLCCGDD 320
Db 02 GDYKRTLLLLCGGDD 316
RESULT 9
Q8CEX0 PRELIMINARY; PRT; 476 AA.
AC Q8CEX0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin A6.
GN ANXA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK010342; BAC25291.1; --
DR MGD; MGI:88255; Anxa6
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 6.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 6.
DR SMART; SM00335; ANX; 5.
DR PROSITE; PS00223; ANNEXIN; 5.
SQ SEQUENCE 476 AA; 53669 MW; 9390C5B5E6653D24 CRC64;
Query Match 58.9%; Score 942; DB 11; Length 476;
Best Local Similarity 59.4%; Pred. No. 1.1e-59;
Matches 187; Conservative 48; Mismatches 80; Indels 0; Gaps 0;
QY 6 RGTVPDPPGDERADATLRKAMKGLGTDEESILTILTSRSNAQOEISAAFKTLFGDRL 65
Db 11 RGSVHDFPEFDANQDAEALYAMKGFSGDKESITLTSRSNAQOEISAAFKTLHGKDL 70
QY 66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db 71 IEDLKVELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 130
QY 126 KQVVEEYSGSLEDVVGDTSGYYQYRMVLLQANRPDPADAGIDEAQVEQDAQALFQAGEL 185

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Db 131 VAAVKDAYERDLESIIIGTSGHFKQMLVLLQGTRENDVVSDDLVOQDLYEAGEL 190
Qy 186 KWTDEEKFTITFGTRSVSHLRKVPDKWTISGGQIBETIDRETSGNLEQLLAVVKISIR 245
Db 191 KWTDEAQFIYILGNRSKQHLRLVFEYKLTGTPKPIEASIREELSGDFEKLMLAVVKIR 250
Qy 246 SIPAYLAETLYYAMKAGCTDDHTLIRVMSVSRSEIDLNFIRKFRKNFATSLYSIMIKGDT 305
Db 251 STPEYFAERLFCAMKGLGTRDNTLIRVMSRSELDMLDIRFRTKYEKSLSYMIKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 10
Q99JX6
ID Q99JX6 PRELIMINARY; PRT; 667 AA.
AC Q99JX6;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Similar to annexin A6.
GN ANXA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: CONTAINS 8 ANNEXIN REPEATS.
DR EMBL; BC005595; AA05595.1; -.
DR HSP; P79134; IAVC.
DR MGD; MGI:88255; Anxa6.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PRO0196; ANNEXIN.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 8.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 667 AA; 75260 MW; 363088A2A55CF34 CRC64;

Query Match 58.9%; Score 942; DB 11; Length 667;
Best Local Similarity 59.4%; Pred. No. 1.8e-59;
Matches 187; Conservative 49; Mismatches 79; Indels 0; Gaps 0;

Qy 6 RGVTDPPGDERADAETLRKAMKGLGTDDEESILTLTSRQAQOEISAAPKTLFGRDL 65
Db 11 RGSVHDFPFDDANQDAEALYTAMKFGSGDKESILELITSRNKRQOEICQYSKYGKDL 70
Qy 66 LDDLKSELTKGPKELIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPELRAI 125
Db 71 IEDLKVELTKGPKELIVNMRPLAYCDAKEIKDAISGIGTDEKCLTEILASRTNEQMHQL 130
Qy 126 KQVVEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 131 VAAVKDAYERDLESIIIGTSGHFKQMLVLLQGTRENDVVSDDLVOQDLYEAGEL 190
Qy 186 KWTDEEKFTITFGTRSVSHLRKVPDKWTISGGQIBETIDRETSGNLEQLLAVVKISIR 245
Db 191 KWTDEAQFIYILGNRSKQHLRLVFEYKLTGTPKPIEASIREELSGDFEKLMLAVVKIR 250
Qy 246 SIPAYLAETLYYAMKAGCTDDHTLIRVMSVSRSEIDLNFIRKFRKNFATSLYSIMIKGDT 305
Db 251 STPEYFAERLFCAMKGLGTRDNTLIRVMSRSELDMLDIRFRTKYEKSLSYMIKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 12
Q7TMN7
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Db 251 STPEYFAERLFCAMKGLGTRDNTLIRVMSRSELDMLDIRFRTKYEKSLSYMIKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 11
Q8BSS4
ID Q8BSS4 PRELIMINARY; PRT; 673 AA.
AC Q8BSS4;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Annexin A6.
GN ANXA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA The FANTOM Consortium,
RA STRAIN=C57BL/6J; TISSUE=Body;
RA MEDLINE=22354683; PubMed=12466851;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030728; BAC27101.1; -.
DR MGD; MGI:88255; Anxa6.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PRO0196; ANNEXIN.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 8.
SQ SEQUENCE 673 AA; 75885 MW; DCC5FC56CDB88809 CRC64;

Query Match 58.8%; Score 940; DB 11; Length 673;
Best Local Similarity 59.4%; Pred. No. 2.5e-59;
Matches 187; Conservative 48; Mismatches 80; Indels 0; Gaps 0;

Qy 6 RGVTDPPGDERADAETLRKAMKGLGTDDEESILTLTSRQAQOEISAAPKTLFGRDL 65
Db 11 RGSVHDFPFDDANQDAEALYTAMKFGSGDKESILELITSRNKRQOEICQYSKYGKDL 70
Qy 66 LDDLKSELTKGPKELIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPELRAI 125
Db 71 IEDLKVELTKGPKELIVNMRPLAYCDAKEIKDAISGIGTDEKCLTEILASRTNEQMHQL 130
Qy 126 KQVVEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 131 VAAVKDAYERDLESIIIGTSGHFKQMLVLLQGTRENDVVSDDLVOQDLYEAGEL 190
Qy 186 KWTDEEKFTITFGTRSVSHLRKVPDKWTISGGQIBETIDRETSGNLEQLLAVVKISIR 245
Db 191 KWTDEAQFIYILGNRSKQHLRLVFEYKLTGTPKPIEASIREELSGDFEKLMLAVVKIR 250
Qy 246 SIPAYLAETLYYAMKAGCTDDHTLIRVMSVSRSEIDLNFIRKFRKNFATSLYSIMIKGDT 305
Db 251 STPEYFAERLFCAMKGLGTRDNTLIRVMSRSELDMLDIRFRTKYEKSLSYMIKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325
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ID	Q7T391	PRELIMINARY;	PRT;	483 AA.
AC	Q7T391;			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=Kidney;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzyszinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Strausberg R.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC053208; AAH53208.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 483 AA; 51425 MW; E4F7F527E30F6DD7 CRC64;			
Query Match 57.2%; Score 915; DB 13; Length 483;				
Best Local Similarity 57.5%; Pred. No. 9.8e-58;				
Matches 181; Conservative 53; Mismatches 81; Indels 0; Gaps 0;				
Qy	6	RGVTDFPGFDERADAETLRKAMKGLGTDEESITLLTSRNAQRQEISAAFKTLFGDRL	65	
Db	169	RGSIQDFPGADPLRDAEVLKAMKGFDTDEQAIIINLGSRSNKQRFVLLSYKTAYGKOL	228	
Qy	66	LDLKLSELTKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIATSTPEELRAI	125	
Db	229	IKDLKSELGNFEKVLAMLKTPSQDAYELKAIKAGTDEACLIILASRSNAEIREI	288	
Qy	126	KQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL	185	
Db	289	NOVFKAENKKSLEDAISGDTSGHFRLLVSLAQNDESENVDISTAKTDQALYQAGEN	348	
Qy	186	KWGTDEEKFTITFGTSVSHLRKRVKDYMTISGQIEETIDRETSGNLEQLLAVVKSIR	245	
Db	349	KLGTDSKFNAILCARSKAHLRAVFNEYQHMCGRDIEKSIEREMSGDLESGMLAVVKCIK	408	
Qy	246	STPAYLAETLYAMKAGTDDHTLIRVMSVRSSEIDLFNIRKEFRKNFATSLYSIMKIGDTS	305	
Db	409	NTPAYFAERLHKAMKAGTKDRTLIRIMVTRSEVMDLIRQYAKNYGKSLYTAISGDT	468	
Qy	306	GDYKALLLLCGEDD	320	
Db	469	GDYKLLKLLCGSD	483	

7	PRELIMINARY;	PRT;	319 AA.
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OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99025617; PubMed=9809745;
RX Osterloh D., Wittbrodt J., Gerke V.;
RT "Characterization and developmentally regulated expression of four
RL annexins in the killifish medaka.";
RN DNA Cell Biol. 17:835-847(1998).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
CC EMBL; Y11252; CAA72122.1; -.
DR HSP; P13214; IANN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00131; annexin; 4.
DR PRINTS; PR06196; ANNEXIN.
DR ProDom; PD060143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 320 AA; 35424 MW; D2EED32C867677D CRC64;

Query Match 54.8%; Score 876; DB 13; Length 320;
Best Local Similarity 54.8%; Pred. No. 3.5e-55;
Matches 171; Conservative 59; Mismatches 82; Indels 0; Gaps 0

Qy 6 RGVTDPFGDERADARTLRKAMKGLGTDEBSILTLLTSRSNAQRQEISAAFKTLFGRDL 65
Db |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
7 RGVVTEASGPNPDDDAQKLREAMKGAGTDEAAIKVLAHRTIAQRRIKLAYKQSVGKDL 66
Yy :|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
67 AEULSSLSGHFSQVVLGLMPAPVYDAYELKAAMKGATGEACLDILASKNSEMNAI 126
Qy :|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
126 KQVVEEYGGSLDDVVVDGTSGYGYRQLMVLVLLQANRPDAGIDEAQVBQDAQALFQAGEL 185
Db |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
127 NEVKYKYGKTLEDAVGCDTSGMFQRVLVSLLTAGRDESQVDEAQAVKADAKIPEAGEA 186
Qy :|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
186 KWGTDESEKFITIFGTRSVSHLRKVDFKYMTISGFQIEETIDRETSGNLEQLLAVVKSIK 245
Db |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
187 RWGTDVEKFTIVLCVRNNHLLRVFDEYKKISKRDIEDSKREMSSGSDVEDFLAVKCLR 246
Qy :|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
246 SIPAYLAETLYAMKGATGDHTLIIRVMVSSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
Db |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
247 SKPAFFAEERLYKSMKGLTTDSVLIRIMVSRAEIDMLDKHEFLTKYGKLSHSFIKGDTS 306
Qy :|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
306 GDYKKALLLCG 317
Db |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
307 GDYRKILLELCG 318

RESULT 16
ID O93447 PRELIMINARY; PRT; 508 AA.
AC O93447;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin max4.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Telostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99025617; PubMed=9809745;
RX Osterloh D., Wittbrodt J., Gerke V.;
```


cterization and developmentally regulated expression of four
ns in the killifish medaka.",
ll Biol. 17:835-847(1998).
MAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
LCTUM AND PHOSPHOLIPID (BY SIMILARITY).
MILARITY: BELONGS TO THE ANNEXIN FAMILY.
MILARITY: CONTAINS 4 ANNEXIN REPEATS.
Y11255: CAA72125.1; -.
P79134; IAVC.
:0005509; F:calcium ion binding; IEA.
ro; IPR001464; F:calcium-dependent phospholipid binding; IEA.
ro; IPR001464; Annexin.
ro; IPR006031; XYPPX.
PF00191; annexin; 4.
PF02162; XYPPX; 15.
; PD00196; ANNEXIN.
; PD000143; Annexin; 4.
SM00335; ANX; 4.
E; PS00223; ANNEXIN; 4.
n; Calcium; Calcium-binding; Calcium/phospholipid-binding;
CE 508 AA; 53051 MW; 3C6728D475CAE430 CRC64;
ch 54.1%; Score 866; DB 13; Length 508;
l Similarity 55.6%; Pred. No. 3.6e-54;
175; Conservative 51; Mismatches 89; Indels 0; Gaps 0;
6 RGTVDPPGDERADAETLRKAMKGLTDEESILTLTSSNAQROEISAAFKTLFGDRL 65
94 RGSIKDPFGADPLRDVEVLKAMKGFDTDEKAIIEILLGNTRKQRPVPLAAAYKTYGKOL 253
66 LDDKSELTKCKPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRPEELRAI 125
54 FRLKSELTKGFEDLVVAMLKTPQDPAELRAIKAGTDEACLEIILSSRNAEIKI 313
26 KQYEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185
14 NKVYKAEYKGLTDESSDTSCHFRLLVSLCQGNRDERETVDSIAKQDAQKLYAAGEN 373
86 KWTDEKFTITFGTRSVSHLRKVFQKMTISGQIEETIDRETSGNLEOLLAVVKSIR 245
74 KVTDESQFNAILCARSKPHLRVAFHEYQMCCKEIEKISCRETSNLEDGMVAVVKCIR 433
46 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKPFATSLYSMIKGDTS 305
34 NTPAYFAERLHRKAMKAGTKDRTLIRVMVSRSEVMDLIRQEYLRLFGKSLYTHISGDT 493
06 GDYKXALLLCGEDD 320
94 GDYKXALLLCGSSD 508
PRELIMINARY; PRT; 485 AA.
-2003 (TrEMBLrel. 24, Created)
-2003 (TrEMBLrel. 24, Last sequence update)
-2003 (TrEMBLrel. 25, Last annotation update)
n 11b.
danio rerio (Zebrafish) (Danio rerio).
ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
pterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
idae; Danio.
axID=7955;
CE FROM N.A.
S.A.; Olson E.S.; Halpern M.E.;
ebrafish Annexin (Gene Family).";
Res. 0:0-0(2003).
AY178802; AAC02076.1; -.
:0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.

DR InterPro; IPR001464; Annexin.
DR InterPro; IPR006031; XYPPX.
DR Pfam; PF00191; annexin; 4.
DR Pfam; PF02162; XYPPX; 9.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
SQ SEQUENCE 485 AA; 51461 MW; 59D4EE05C4FA253C CRC64;
Query Match 53.9%; Score 862; DB 13; Length 485;
Best Local Similarity 54.9%; Pred. No. 6.6e-54;
Matches 173; Conservative 53; Mismatches 89; Indels 0; Gaps 0;
QY 6 RGTVDPPGDERADAETLRKAMKGLTDEESILTLTSSNAQROEISAAFKTLFGDRL 65
Db 171 RGTIKDPFGADPLRDVEVLKAMKGFDTDEKAIIEILLGNTRKQRPVPLAAAYKTYGKOL 230
QY 66 LDDKSELTKCKPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRPEELRAI 125
Db 231 VRDLKSELTKHPEELVLA MLKSPAQFDASECKEAIISAGTDEACLEIILSSRNAEIKI 290
QY 126 KQYEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185
Db 291 NRIYKAEYKGLSLEDAISNDTSGHFRLLVSLCQGNRDERETVDSIAKQDAQKLYAAGEN 350
QY 186 KWTDEKFTITFGTRSVSHLRKVFQKMTISGQIEETIDRETSGNLEOLLAVVKSIR 245
Db 351 KVTDESQFNAILCARSKPHLRQVFOEYQMCGRDIEKISCREMSGDLSEGMVAVVKCIR 410
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKPFATSLYSMIKGDTS 305
Db 411 NTPAYFAERLHRKAMKAGTKDRTLIRVMVSRSELDMLDIRQEYLRLFGKSLYTHISGDT 470
QY 306 GDYKXALLLCGEDD 320
Db 471 GDYKXALLLCGSSD 485
RESULT 18
Q90X16 PRELIMINARY; PRT; 321 AA.
AC Q90X16; PRELIMINARY; PRT; 321 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin 4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_SEQUENCE FROM N.A.
RP Seville R.A., Nijjar S., Barnett M.W., Jones E.A.;
RA "Annexin 4 (Xanx-4) has a role in the development of the pronephric
RT tubules in Xenopus laevis."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AY039235; AAK83461.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
Repeat.

QY 187 WGTDEBKFTITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIRS 246
 DB 194 CGTDEMKFTITLCTRSARHLRMVFEYKIANKSIEDSIKSETHGSLEBAMLTIVKCTRN 253
 QY 247 IPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEPRKNFATSLYSMIKGDTS 306
 DB 254 LHGYFAERLYAMKAGTDLGTLIRNIVSRSEIDLNLKRNQKMYGKTLSSMIMEDTSG 313
 QY 307 DYKKAALLCGED 319
 DB 314 DYKNALLNLVGS 326

RESULT 23
 O97529 PRELIMINARY; PRT; 327 AA.
 AC O97529;
 DT 01-MAY-1999 (T:EMBLrel. 10, Created)
 DT 01-MAY-1999 (T:EMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (T:EMBLrel. 25, Last annotation update)
 DE Annexin VIII.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng W., Tsao F.H.C.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF012745; AAD01508.1; -
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 SQ SEQUENCE 327 AA; 36680 MW; 1815B77B6BE50AB7 CRC64;

Query Match 51.5%; Score 823.5; DB 6; Length 327;
 Best Local Similarity 55.9%; Pred. No. 2.2e-51;
 Matches 175; Conservative 48; Mismatches 89; Indels 1; Gaps 1;

QY 8 TVTDPFGERADAETLRKAMKGLTGDEESILTLTSRNSAQRQESIAAFKTLFGDRLD 67
 DB 14 TVKGSFHPNPVPAETLYKAMKIGTNEQAIIDVLTTRSSAQRTAKSFKAQFGSDLTE 73
 QY 68 DLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIRASRTPEELRAIKQ 127
 DB 74 TLKSELUSGKFERLIIVALKMPPYRYEAKELHDAKMGKLGTEGVIIIEILASRTNQLQEIIMK 133
 QY 128 VVEEYEGSSLEDDVVGDTSGYORMLVLLQANRDPDAG- IDBAQVEQDAQALFOAGELK 186
 DB 134 AVEEDYGGSSLEDDI QADTSGYLERILVCLQSRDDVTGFDVPGALQAQOLYAGEKI 193
 QY 187 WGTDEBKFTITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIRS 246
 DB 194 CGTDEMKFTITLCTRSARHLRMVFEYKIANKSIEDSIKSETHGSLEBAMLTIVKCTRN 253
 QY 247 IPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEPRKNFATSLYSMIKGDTS 306
 DB 254 LHGYFAERLYAMKAGTDLGTLIRNIVSRSEIDLNLKRNQKMYGKTLSSMIMEDTSG 313
 QY 307 DYKKAALLCGED 319
 DB 314 DYKNALLNLVGS 326

RESULT 24
 O981X9 PRELIMINARY; PRT; 323 AA.
 ID O981X9

AC O981X9;
 DT 01-MAR-2003 (T:EMBLrel. 23, Created)
 DT 01-MAR-2003 (T:EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T:EMBLrel. 25, Last annotation update)
 DE Annexin A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK090055; BAC41070.1; -
 DR MGD; MGI:1201378; Anxa3.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 SQ SEQUENCE 323 AA; 36356 MW; 9F69F57BCFAC6A85 CRC64;

Query Match 50.6%; Score 809; DB 11; Length 323;
 Best Local Similarity 49.5%; Pred. No. 2.4e-50;
 Matches 156; Conservative 63; Mismatches 96; Indels 0; Gaps 0;

QY 6 RGTVDTPFGERADAETLRKAMKGLTGDEESILTLTSRNSAQRQESIAAFKTLFGDRL 65
 DB 9 RGTIKDYPGSPVDAEAIKRAIRKGLTGDEKTLINILTERSNAQRQIAKQYAAVEQEL 68
 QY 66 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIRASRTPEELRAI 125
 DB 69 KDDLKGLDLSGHFEHVWVALVTAPALFDKQLKSKMKGTDDEDALEIILTLTSSRQMKEI 128
 QY 126 KQVVEEYEGSSLEDDVVGDTSGYORMLVLLQANRDPDAGIDBAQVEQDAQALFOAGEL 185
 DB 129 SOAYTVTVKSLGDDISSETSGDFPKALLTLADGRDSESLKVDHKLAKKDAQILYNAGEN 188
 QY 186 KWTDEBKFTITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIR 245
 DB 189 KWTDEBKFTITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIR 248
 QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEPRKNFATSLYSMIKGDTS 305
 DB 249 NTPFLAERLHQALKGAGTDEFTLNRINVSREIDLLDIRHEFKKHGYGSLYSATQSDTS 308
 QY 306 GDYKKAALLCGED 320
 DB 309 GDRVTLLKIGCEDD 323

RESULT 25
 O922A2 PRELIMINARY; PRT; 463 AA.
 ID O922A2
 AC O922A2;
 DT 01-DEC-2001 (T:EMBLrel. 19, Created)
 DT 01-DEC-2001 (T:EMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (T:EMBLrel. 25, Last annotation update)
 DE Annexin A7.
 GN ANXA7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

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99 643 40.2 346 2 AAP06560 Human 1ip
100 642 40.1 345 7 ADE60115 Human Pro

ALIGNMENTS

RESULT 1

AAP80511

ID AAP80511 standard; protein; 320 AA.

XX AAP80511;

XX AC 25-MAR-2003 (revised)

XX DT 10-MAR-2003 (revised)

XX DT 12-NOV-1990 (first entry)

XX DE Placental coagulation inhibitor.

XX KW Placental coagulation inhibitor; disseminated vascular coagulation;

XX KM thrombosis.

XX OS Homo sapiens.

XX PN EP279459-A.

XX PD 24-AUG-1988.

XX PF 19-FEB-1988; 88EP-00102468.

XX PR 20-FEB-1987; 87JP-00037227.

XX PR 23-JUL-1987; 87JP-00184428.

XX PA (KOMA) KOMA CO LTD.

XX PI Saino Y, Iwasaki A, Suda M;

XX DR WPI; 1988-236733/34.

XX DR N-PSDB; AAN81113.

XX PT Recombinant placental coagulation inhibitor - useful for the prevention
XX and treatment of thromboses or disseminated intravascular coagulation.

XX PS Disclosure; Page ?; 31pp; English.

XX CC This polypeptide exhibits strong anticoagulant activities and is useful

XX CC for the treatment and prevention of e.g. thrombosis or disseminated

XX CC intravascular coagulation in the brain, heart and peripheral blood

XX CC vessels, such as cerebral and myocardial infarction. It has no

XX CC antigenicity against man and can be produced in large ams. using

XX CC recombinant methods. (Updated on 10-MAR-2003 to add missing CS field.)

XX CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to

XX CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 320 AA;

XX Query Match 100.0%; Score 1600; DB 1; Length 320;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-134; Indels 0; Gaps 0;

XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DB 1 MAOVLRGVTFDPFGRADAEITLRKAMKGLGTDEESILTLTLTSRSNAQREISAAPKTL 60

XX QY 61 FGRDLDDLKSELNGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120

XX DB 61 FGRDLDDLKSELNGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120

XX QY 121 ELRAIKQYEEYSSLEDVVGDTSGYQMLVVLQANRDPDAGIDEAQBODQAQLF 180

XX DB 121 ELRAIKQYEEYSSLEDVVGDTSGYQMLVVLQANRDPDAGIDEAQBODQAQLF 180

XX QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKMTISGQIEFTIDRETSNLEQLLAV 240

DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKMTISGQIEFTIDRETSNLEQLLAV 240

QY 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWMSRSEIDFNIRKEFRKNFATSLYSMI 300

DB 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWMSRSEIDFNIRKEFRKNFATSLYSMI 300

QY 301 KGDTSGDYKKALLLLCGEDD 320

DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 2

AAP91953

ID AAP91953 standard; protein; 320 AA.

XX AAP91953;

XX AC 24-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 10-MAR-2003 (revised)

XX DT 30-JUL-1989 (first entry)

XX DE Vascular anti-coagulating protein-alpha.

XX KW Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.

XX OS Homo sapiens.

XX OS Mus musculus.

XX OS Chimeric.

XX PN DE3810331-A.

XX PD 05-OCT-1989.

XX PF 26-MAR-1988; 88DE-03810331.

XX PR 26-MAR-1988; 88DE-03810331.

XX PA (BOEH) BOEHRINGER INGELHEIM.

XX PI Gunther A;

XX DR WPI; 1989-293724/41.

XX DR N-PSDB; AAN91353.

XX PT Monoclonal antibodies to vascular anti-coagulating proteins - and
XX hybridomas producing such antibodies.

XX PS Disclosure; Fig 1; 11pp; German.

XX CC This vascular anti-coagulating protein (VAC)-alpha is used in the

XX CC preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected

XX CC into a host animal, in conjunction with eg keyhole limpet haemocyanin,

XX CC and the B-cells from immunised hosts are then fused with myeloma cells.

XX CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-

XX CC alpha. Abs can be used as immunoassay reagents to detect VAC proteins, as

XX CC affinity ligands for protein purification, and as medicaments for binding

XX CC and/or neutralising VAC proteins in vivo. See also AAN91354 and BP-

XX CC 181465. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-

XX CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS

XX SQ Sequence 320 AA;

XX Query Match 100.0%; Score 1600; DB 1; Length 320;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-134; Indels 0; Gaps 0;

XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DB 1 MAOVLRGVTFDPFGRADAEITLRKAMKGLGTDEESILTLTLTSRSNAQREISAAPKTL 60

XX QY 1 MAOVLRGVTFDPFGRADAEITLRKAMKGLGTDEESILTLTLTSRSNAQREISAAPKTL 60

QY 61 FGRDLDDLKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 DB 61 FGRDLDDLKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 QY 121 ELRAIKQYEEERYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 DB 121 ELRAIKQYEEERYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 QY 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVPFKWMTISGFQIEETIDRETSGNLEQLLLA 240
 DB 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVPFKWMTISGFQIEETIDRETSGNLEQLLLA 240
 QY 241 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKPAFATSLYSM 300
 DB 241 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKPAFATSLYSM 300
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 3

AA13082
 ID AA13082 standard; protein; 320 AA.

AC AA13082;
 XX

DT 25-MAR-2003 (revised)
 DT 30-SEP-1991 (first entry)

XX
 DE PAP-I.

XX
 KM Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;
 KM gla-domain; VKDP.

XX
 OS Homo sapiens.

XX
 PN WO9109953-A.

XX
 PD 11-JUL-1991.

XX
 PF 29-DEC-1989; 89US-00459082.

XX
 PR 29-DEC-1989; 89US-00459082.

XX
 PA (ZYMO) ZYMOGENETICS INC.

XX
 PI Foster DC;

XX
 DR WPI, 1991-222905/30.

XX
 DR N-PSDB; AAQ12679.

PT Recombinant prodn. of hybrid phospholipid-binding proteins - comprising
 PT lipocortin phospholipid-binding domain and vitamin-K-dependent protein.

XX
 PS Disclosure; Fig 7; 5pp; English.

XX
 CC This sequence, or a fragment of it, is used in the construction of hybrid
 CC phospholipid-binding proteins (PBP) comprising at least one lipocortin
 CC phospholipid-binding domain (PBD), e.g. of PAP-I, joined to a gla-
 CC domainless vitamin K-dependent protein, e.g. protein C or activated
 CC protein C. See AAQ12680-81 for such examples. See also AAQ12678-81.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 320 AA;

QY Query Match

Best Local Similarity 100.0%; Score 1600; DB 2; Length 320;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPPFDERADAEETLRKAMKGLGTDEESITLTLTSRSNAQROEISAAPKTL 60
 DB 1 MAQVLRGTVDPPFDERADAEETLRKAMKGLGTDEESITLTLTSRSNAQROEISAAPKTL 60

QY 61 FGRDLDDLKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 DB 61 FGRDLDDLKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 QY 121 ELRAIKQYEEERYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 DB 121 ELRAIKQYEEERYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 QY 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVPFKWMTISGFQIEETIDRETSGNLEQLLLA 240
 DB 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVPFKWMTISGFQIEETIDRETSGNLEQLLLA 240
 QY 241 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKPAFATSLYSM 300
 DB 241 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKPAFATSLYSM 300
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 4

AA13923
 ID AA13923 standard; protein; 320 AA.

AC AA13923;
 XX

DT 13-JUL-1999 (first entry)

XX
 DE S65T GFP variant/annexin V protein.

XX
 KM GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KM fluorescent intensity; anionic phospholipid binding affinity;
 KM asymmetric distribution; plasma membrane phospholipid;
 KM apoptotic cell detection.

XX
 OS Aequorea victoria.

XX
 OS Homo sapiens.

XX
 OS Synthetic.

XX
 PN WO9199470-A2.

XX
 PD 22-APR-1999.

XX
 PF 09-OCT-1998; 98WO-US021444.

XX
 PR 09-OCT-1997; 97US-00948276.

XX
 PA (REGC) UNIV CALIFORNIA.

XX
 PI Ernst JD;

XX
 DR WPI, 1999-277634/23.

PT Bifunctional fusion protein useful for the detection of apoptotic cel

XX
 PS Claim 2; Page 14-15; 23pp; English.

XX
 CC This sequence represents an example of a protein of the invention. The
 CC proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties proin
 CC greater or equal fluorescent intensity and anionic phospholipid bindi
 CC affinity, respectively, than do the corresponding unfused GFP and ann
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which result
 CC in exposure of anionic phospholipids on the extracellular leaflet of t
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microsc
 CC fluorescence properties that do not change upon binding annexin, with
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenchin
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholip

CC 1 MAQVLRGTVDPPFDERADAEETLRKAMKGLGTDEESITLTLTSRSNAQROEISAAPKTL 60
 CC 1 MAQVLRGTVDPPFDERADAEETLRKAMKGLGTDEESITLTLTSRSNAQROEISAAPKTL 60

CC	membranes	Sequence	320 AA;	100.0%; Score 1600; DB 2; Length 320;	Best Local Similarity 100.0%; Pred. No. 1.3e-134; Mismatches 0; Indels 0; Gaps 0
XX	XX	Query Match			
XX	XX	Matches 320; Conservative			
QY	1	MAQVIRGVYTPDPGDERADAEFLRKAMKGLGTDSEIITLLTSRSNAQROEISAAFKTL	60		
DB	1	MAQVIRGVYTPDPGDERADAEFLRKAMKGLGTDSEIITLLTSRSNAQROEISAAFKTL	60		
QY	61	FGRLDLDLKSLELTGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKYLTEIIASRTPE	120		
DB	61	FGRLDLDLKSLELTGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKYLTEIIASRTPE	120		
QY	121	ELRAIKQVVEEYEGSSLEDVVDVDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF	180		
DB	121	ELRAIKQVVEEYEGSSLEDVVDVDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF	180		
QY	181	QAGELKMGTDDEEKFTITFGTRSVSHLRKVPDKYMTISGFOIETITDRETSGNLJQLLLAV	240		
DB	181	QAGELKMGTDDEEKFTITFGTRSVSHLRKVPDKYMTISGFOIETITDRETSGNLJQLLLAV	240		
QY	241	VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKNFATSLYSMI	300		
DB	241	VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKNFATSLYSMI	300		
QY	301	KGDTSGDYKKALLLCGEDD 320			
DB	301	KGDTSGDYKKALLLCGEDD 320			
XX	XX	RESULT 5			
XX	XX	AA84788			
XX	XX	AA84788 standard; peptide; 320 AA.			
XX	XX	AA84788;			
XX	XX	08-AUG-2000 (first entry)			
XX	XX	Amino acid sequence of annexin V.			
XX	XX	Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory;			
XX	XX	KM coacting; thrombogenic biomaterial; labelling compound; negative charge.			
XX	XX	Unidentified.			
XX	XX	Key	Location/Qualifiers		
XX	XX	Domain	16..91		
XX	XX		/note="domain 1"		
XX	XX	FR2784106-A1.			
XX	XX	07-APR-2000.			
XX	XX	02-OCT-1998; 98PR-00012366.			
XX	XX	02-OCT-1998; 98PR-00012366.			
XX	XX	02-OCT-1998; 98PR-00012366.			
XX	XX	(COMS) COMMISSARIAT ENERGIE ATOMIQUE.			
XX	XX	(UYPA-) UNIV CURIE PARIS VI P & M.			
XX	XX	Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerois R;			
XX	XX	WPI; 2000-320664/28.			
XX	XX	Chemical structure having affinity for phospholipid comprises chemical			
XX	XX	platform comprising six residues supporting set of chemical functions			
XX	XX	that are capable of binding to phospholipid.			
XX	XX	Claim 13; Fig 6b; 63pp; French.			

The present sequence represents an annexin polypeptide. The domain of CC annexin, which may be modified, is used to construct the chemical compounds of the invention. The specification describes chemical compounds which have an affinity for a phospholipid. The chemical compounds comprise at least one chemical platform comprising six residues supporting a set of chemical functions that are capable of binding to the phospholipid and at least partly define the affinity of the structure for the phospholipid. The compounds act as phospholipid sequestrers. The compounds are useful for preparing antithrombotic, anticancer and antiinflammatory medicaments, for making coatings for thrombogenic biomaterials, and for preparing labelling compounds useful for analysing and detecting negative charges on cell surfaces and microvesicles in blood.

Sequence 320 AA:

Query Match 100.0%; Score 1600; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.3e-134;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAQVLRGVTVPFGPDERADAEYLTKAMKGLGTDESIILTLTSSNSNAQROEISAAPKTL 60
1 MAQVLRGVTVPFGPDERADAEYLTKAMKGLGTDESIILTLTSSNSNAQROEISAAPKTL 60

61 FGRDLDDLLKSELTKGFPEKLIYALMKPSRLYDAYELKALKGAGTNEKYLTEIISRTPE 120
61 FGRDLDDLLKSELTKGFPEKLIYALMKPSRLYDAYELKALKGAGTNEKYLTEIISRTPE 120

121 ELRAIKQVVEEYEGSSLEDDVVGDTSGYYQRMVLVLQANRPDAGIDEAQVEQDAQALF 180
121 ELRAIKQVVEEYEGSSLEDDVVGDTSGYYQRMVLVLQANRPDAGIDEAQVEQDAQALF 180

181 QAGELKMGTDDEKFTTIFGTRSVSHLRKPFDMKYMTISGQIETIDRETSGNLEQLLAV 240
181 QAGELKMGTDDEKFTTIFGTRSVSHLRKPFDMKYMTISGQIETIDRETSGNLEQLLAV 240

241 VKSIRSIPIAYLAETLYYAMKGAETDHTLIRVWVSRSEIDLFNIRKPEKKNFATISLSMI 300
241 VKSIRSIPIAYLAETLYYAMKGAETDHTLIRVWVSRSEIDLFNIRKPEKKNFATISLSMI 300

301 KGDTSQDYKKALLLGCEDD 320
301 KGDTSQDYKKALLLGCEDD 320

RESULT 6
ABG31220
ID ABG31220 standard; protein; 320 AA.

ABG31220;
05-NOV-2002 (first entry)

Human annexin V, containing a delta RACK binding site.

Human, annexin V, delta RACK; delta protein kinase C; deltaPKC;
VI domain; vasotrophic; cerebroprotective; deltaV1-1; deltaV1-2; RACK;
pseudo-delta RACK; pseudo-delta receptor for activated C-kinase;
deltaV1-5; PKC; protein kinase C; signal transduction; cell growth;
gene expression; ion channel activity; translocation; hypoxia; stroke;
ischaemic damage; creatine kinase.

Homo sapiens.
WO200257413-A2.
25-JUL-2002.
09-NOV-2001; 2001WO-US047556.
18-JAN-2001; 2001US-0262060P.
(STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;
XX

DR WPI: 2002-599715/64.

PT New delta protein kinase C peptide for reducing or enhancing damage to
PT cells or tissues exposed to ischemic or hypoxic event caused by stroke,
XX or for protecting tissue from damage due to ischemia.

PS Claim 45; Page 64-65; 65pp; English.

XX The invention discloses peptides comprising deltaV1-1, deltaV1-2, pseudo-
CC delta receptors for activated C-kinase (RACK), deltaV1-5 or their
CC derivatives or fragments. Protein kinase C (PKC) is a key enzyme in
CC signal transduction involved in a variety of cellular functions including
CC cell growth, regulation of gene expression and ion channel activity. The
CC localisation of different PKC isozymes to different areas of the cell in
CC turn appears due to binding of the activated isozymes to the specific
CC anchoring molecules (RACKs). Peptides that mimic either the PKC-binding
CC site on RACKs or the RACK-binding site on PKC are isozyme specific
CC translocation inhibitors of PKC. The disclosed peptides are useful in
CC activating or inhibiting translocation or function of deltaPKC. The
CC deltaPKC agonists or antagonists are useful in reducing, enhancing or
CC protecting against damage to cells or tissues due to ischaemic or hypoxic
CC event caused by stroke. Acute administration of the peptides, conjugated
CC to a carrier peptide or a Tat-derived peptide, protected hearts against
CC ischaemic damage as shown by decreased release of creatine kinase. The
CC data indicate that in an intact heart, inhibition of deltaPKC conferred
CC greater than 50% protection against ischaemic damage. The sequence
CC presented is human annexin V, which contains a delta RACK binding site
XX

SO Sequence 320 AA;

Query Match 100.0%; Score 1600; DB 5; Length 320;
Best Local Similarity 100.0%; Pred. No. 1,3e-134;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAQVLRGTTVPFPGFPERADAEFLTRKAMKGLGTDSESIITLTSRSNAQROEISAFAKTL	60
DB	1	MAQVLRGTTVPFPGFPERADAEFLTRKAMKGLGTDSESIITLTSRSNAQROEISAFAKTL	60
QY	61	FGRLDLDLKSSELTGFEKLIYALMKPSRLYDAEYELKHALKAGTNEKVLTEIIASRTPE	120
DB	61	FGRLDLDLKSSELTGFEKLIYALMKPSRLYDAEYELKHALKAGTNEKVLTEIIASRTPE	120
QY	121	ELRAIKQVVEEYSGSSLEDVVGDTSGYQRMVLVLLQNNRDPDAGIDEAQVEQDAQALF	180
DB	121	ELRAIKQVVEEYSGSSLEDVVGDTSGYQRMVLVLLQNNRDPDAGIDEAQVEQDAQALF	180
QY	181	QAGELKMGTDSEKFTITIGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQILLAV	240
DB	181	QAGELKMGTDSEKFTITIGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQILLAV	240
QY	241	VKSIRSIPIAYLAETLYYAMKAGTGDHTLIRVWRSRSEIDLFNIRKPKNPAISLYSMI	300
DB	241	VKSIRSIPIAYLAETLYYAMKAGTGDHTLIRVWRSRSEIDLFNIRKPKNPAISLYSMI	300
QY	301	KGDTSGDYKKAALLLCGEDD 320	
DB	301	KGDTSGDYKKAALLLCGEDD 320	

RESULT 7

ID AAP90053 standard; protein; 320 AA.

XX AAP90053;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE anticoagulant PP4 protein.

XX Anticoagulant; PP4 protein; thromboplastic.
KW
XX Homo sapiens; (human).

OS EP18703-A.

PN 07-JUN-1989.

PD 29-OCT-1988; 88EP-00118039.

XX 03-NOV-1987; 87DE-03737239.

PR (BEHW) BEHRINGER AG.

PA Grundmann U, Abel KJ, Kupper H;

XX WPI: 1989-166767/23.

DR

XX New DNA sequence encoding anticoagulant PP4 protein - and new recomb

PT protein, vectors, antibodies, etc., useful therapeutically and

PT diagnostically.

XX Claim 1, Page 11 and Table 1; 12pp; German.

CC Amino acid sequence of anticoagulant PP4 protein. This inhibits bloo

CC coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to

CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Upd

CC on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to

CC standardise OS field)

CC

XX

SO Sequence 320 AA;

Query Match 99.8%; Score 1597; DB 1; Length 320;
Best Local Similarity 99.7%; Pred. No. 2,5e-134;
Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps

QY	1	MAQVLRGTTVPFPGFPERADAEFLTRKAMKGLGTDSESIITLTSRSNAQROEISAFAKTL	60
DB	1	MAQVLRGTTVPFPGFPERADAEFLTRKAMKGLGTDSESIITLTSRSNAQROEISAFAKTL	60
QY	61	FGRLDLDLKSSELTGFEKLIYALMKPSRLYDAEYELKHALKAGTNEKVLTEIIASRTPE	120
DB	61	FGRLDLDLKSSELTGFEKLIYALMKPSRLYDAEYELKHALKAGTNEKVLTEIIASRTPE	120
QY	121	ELRAIKQVVEEYSGSSLEDVVGDTSGYQRMVLVLLQNNRDPDAGIDEAQVEQDAQALF	180
DB	121	ELRAIKQVVEEYSGSSLEDVVGDTSGYQRMVLVLLQNNRDPDAGIDEAQVEQDAQALF	180
QY	181	QAGELKMGTDSEKFTITIGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQILLAV	240
DB	181	QAGELKMGTDSEKFTITIGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQILLAV	240
QY	241	VKSIRSIPIAYLAETLYYAMKAGTGDHTLIRVWRSRSEIDLFNIRKPKNPAISLYSMI	300
DB	241	VKSIRSIPIAYLAETLYYAMKAGTGDHTLIRVWRSRSEIDLFNIRKPKNPAISLYSMI	300
QY	301	KGDTSGDYKKAALLLCGEDD 320	
DB	301	KGDTSGDYKKAALLLCGEDD 320	

RESULT 8

ID AAY92930 standard; protein; 600 AA.

XX AAY92930;
XX
XX 25-OCT-2000 (first entry)
DT
XX Annexin V/urokinase fusion protein.
DE Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion proteas
KW

KW urokinase; insect cell; fibrinolysis.
 XX Unidentified.
 OS
 XX CN1247195-A.
 PN
 XX
 XX PD 15-MAR-2000.
 XX
 XX PF 12-MAR-1999; 99CN-00113524.
 XX
 XX PR 12-MAR-1999; 99CN-00113524.
 XX
 XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
 XX
 XX PI Wu X, Sun J, Yang G;
 XX
 XX DR MPI: 2000-413098/36.
 XX N-PSDB; AAA11241.
 XX
 XX PT New thrombolytic fusion protein for targeting thrombus - comprises
 XX fusion of Annexin V and urokinase.
 XX
 XX PS Claim 2; Page 2-4; 20pp; Chinese.
 XX
 XX CC Annexin V, which has high affinity for active thrombocytes, is used as a
 XX carrier molecule to build a thrombus-targeting thrombolytic fusion
 XX protein. The protein (this sequence) is the result of expression of a
 XX fusion gene comprising the Annexin V gene and a low-molecular urokinase
 XX gene, in insect cells. The Annexin V-scFv-32 fusion protein, expressed
 XX in insect cell strain "n-5B1-4", has high affinity for active thrombocytes
 XX and has the fibrinolytic activity of urokinase
 XX
 XX SQ Sequence 600 AA;

Query Match 99.8%; Score 1597; DB 3; Length 600;
 Best Local Similarity 99.7%; Pred. No. 5.8e-134;
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAOVLRTGVTFPGFDERADAEITRKAMKGLGIDEESITLTLISRSNAOQETSAAFKTL 60
 DB 281 MAOVLRTGVTFPGFDERADAEITRKAMKGLGIDEESITLTLISRSNAOQETSAAFKTL 340
 OY 61 FGRDLDDLKSELGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
 DB 341 FGRDLDDLKSELGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 400
 OY 121 ELRAIKOYEEYEGSSLEDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEDQAQLF 180
 DB 401 ELRAIKOYEEYEGSSLEDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEDQAQLF 460
 OY 181 OAGELKMGTDDEKFTITFGTSVSHLRKVFDPKMTISGFQIEETIDRETSGNLEQOLLAV 240
 DB 461 OAGELKMGTDDEKFTITFGTSVSHLRKVFDPKMTISGFQIEETIDRETSGNLEQOLLAV 520
 OY 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFINRKEPKKPAFATSLYSMT 300
 DB 521 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFINRKEPKKPAFATSLYSMT 580
 OY 301 KGDTSGDYKKAALLLCGEDD 320
 DB 581 KGDTSGDYKKAALLLCGEDD 600

RESULT 9
 AAP82317
 ID AAP82317 standard; protein; 320 AA.
 XX
 AC AAP82317;
 XX
 XX 25-MAR-2003 (revised)
 DT 13-NOV-1990 (first entry)
 XX
 XX PAP-I isolated from biological fluid, used as anticoagulant.

XX PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;
 KW phospholipase A2; disseminated intravascular coagulation;
 XX deep vein thrombosis.
 XX
 XX OS Homo sapiens.
 XX
 XX PN MO805659-A.
 XX
 XX OS
 XX PD 11-AUG-1988.
 XX
 XX PF 05-FEB-1988; 88WO-US000340.
 XX
 XX PR 06-FEB-1987; 87US-00011782.
 XX PR 05-JUN-1987; 87US-00059355.
 XX
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX (UNIT) UNIT WASHINGTON.
 XX
 XX PI Fujikawa K, Irani MH, Carter BLA;
 XX
 XX DR MPI: 1988-235049/33.
 XX N-PSDB; AAN82107.
 XX
 XX PT Human proteins having anticoagulant and antiinflammatory activity -
 XX isolated from biological fluids by anion-exchange chromatographic media.
 XX
 XX PS Disclosure; Page 7; 62pp; English.

XX The protein does not contain a leader peptide sequence, indicating that
 XX PAP-I is probably not constitutively secreted. The Met residue is removed
 XX at in a post-translational event and the newly formed NH2-terminal Ala
 XX residue is blocked by acetylation. It binds to phospholipid and inhibits
 XX phospholipase A2. The protein can substitute heparin or other
 XX anticoagulants in the treatment of disseminated intravascular
 XX coagulation, deep vein thrombosis, or other disorders. It also has
 XX antiinflammatory properties. (Updated on 25-MAR-2003 to correct PA
 XX field.)
 XX
 XX SQ Sequence 320 AA;

Query Match 99.8%; Score 1596; DB 1; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3e-134;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAOVLRTGVTFPGFDERADAEITRKAMKGLGIDEESITLTLISRSNAOQETSAAFKTL 60
 DB 1 MAOVLRTGVTFPGFDERADAEITRKAMKGLGIDEESITLTLISRSNAOQETSAAFKTL 60
 OY 61 FGRDLDDLKSELGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
 DB 61 FGRDLDDLKSELGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
 OY 121 ELRAIKOYEEYEGSSLEDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEDQAQLF 180
 DB 121 ELRAIKOYEEYEGSSLEDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEDQAQLF 180
 OY 181 OAGELKMGTDDEKFTITFGTSVSHLRKVFDPKMTISGFQIEETIDRETSGNLEQOLLAV 240
 DB 181 OAGELKMGTDDEKFTITFGTSVSHLRKVFDPKMTISGFQIEETIDRETSGNLEQOLLAV 240
 OY 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFINRKEPKKPAFATSLYSMT 300
 DB 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFINRKEPKKPAFATSLYSMT 300
 OY 301 KGDTSGDYKKAALLLCGEDD 320
 DB 301 KGDTSGDYKKAALLLCGEDD 320

RESULT 10
 AAR26276
 ID AAR26276 standard; protein; 319 AA.

XX AC AAR26276;
XX DT 10-MAR-2003 (revised)
XX DT 04-FEB-1993 (first entry)
XX DE CPB-I.
XX KW CPB-I; stabilisation; frozen; molten; processed; activity.
XX OS Homo sapiens.
XX PN JP04198195-A.
XX PD 17-JUL-1992.
XX PF 28-NOV-1990; 90JP-00328286.
XX PR 28-NOV-1990; 90JP-00328286.
XX PA (KOMA) KOMA CO LTD.
XX PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
XX DR WPI; 1992-288937/35.
XX PT Stabilisation of CPB-I for drug compn. - by adding basic aminoacid
XX PT selected from lysine, arginine and/or ornithine.
XX PS Disclosure; Page 2; 4pp; Japanese.
XX CC The sequence given is the amino acid sequence of CPB-I. CPB-I was used
XX CC within a method which involved adding basic amino acids to it which
XX CC resulted in its stabilisation. This lead to the production of CPB-I which
XX CC keeps its activity when it is frozen, molten or has been processed by
XX CC several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
SQ Sequence 319 AA;

Query Match 99.7%; Score 1595; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.7e-134;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AQLVGTVDTPGFDERADAETLRKAMKGLGDEESILTLTSSNAQOEISAAPKTLF 61
DB 1 AQLVGTVDTPGFDERADAETLRKAMKGLGDEESILTLTSSNAQOEISAAPKTLF 60
QY 62 GRDLDDDKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 121
DB 61 GRDLDDDKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 120
QY 122 LRAIKQVYEEYSSLEDDVDPGTSYQRMVLLQANRDPAGIDEAQVEDQAALFQ 181
DB 121 LRAIKQVYEEYSSLEDDVDPGTSYQRMVLLQANRDPAGIDEAQVEDQAALFQ 180
QY 182 AGEKMGTDDEEKFITIFGRSVSHLRKVPDKYMTISGFOEETIDETSNGNEQLLAVV 241
DB 181 AGEKMGTDDEEKFITIFGRSVSHLRKVPDKYMTISGFOEETIDETSNGNEQLLAVV 240
QY 242 KSIRSIPIALAEITLYYAMKAGAGTDHLLIRWVSRSEIDLFINIRKFRKNPATSLYSMTK 301
DB 241 KSIRSIPIALAEITLYYAMKAGAGTDHLLIRWVSRSEIDLFINIRKFRKNPATSLYSMTK 300
QY 302 GDTSGDYKALLLLCGEDD 320
DB 301 GDTSGDYKALLLLCGEDD 319

RESULT 11
ID AAR41021 standard; protein; 319 AA.
XX AAR41021;
XX

DT 29-MAR-1994 (first entry)
XX DE Calphobindin I (CPB-I).
XX KW Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
XX OS Homo sapiens.
XX PN JP05213769-A.
XX PD 24-AUG-1993.
XX PF 04-FEB-1992; 92JP-00019032.
XX PR 04-FEB-1992; 92JP-00019032.
XX PA (KOMA) KOMA CO LTD.
XX PA (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKUTUSHO.
XX DR WPI; 1993-299558/38.
XX PT Protein kinase C inhibitor effective against malignant tumours - con
XX PT (opt. recombinant) calphobindin I.
XX PS Claim 1; Page 2-3; 6pp; Japanese.
XX CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I) inhib
XX CC protein kinase C (PKC) and is useful in the treatment of malignant
XX CC tumours caused by abnormal activation of PKC. CPB-I is extracted from
XX CC human or animal organs and may be applied intravenously, orally,
XX CC intramuscularly, percutaneously or rectally
SQ Sequence 319 AA;

Query Match 99.7%; Score 1595; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.7e-134;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AQLVGTVDTPGFDERADAETLRKAMKGLGDEESILTLTSSNAQOEISAAPKTLF 61
DB 1 AQLVGTVDTPGFDERADAETLRKAMKGLGDEESILTLTSSNAQOEISAAPKTLF 60
QY 62 GRDLDDDKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 121
DB 61 GRDLDDDKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 120
QY 122 LRAIKQVYEEYSSLEDDVDPGTSYQRMVLLQANRDPAGIDEAQVEDQAALFQ 181
DB 121 LRAIKQVYEEYSSLEDDVDPGTSYQRMVLLQANRDPAGIDEAQVEDQAALFQ 180
QY 182 AGEKMGTDDEEKFITIFGRSVSHLRKVPDKYMTISGFOEETIDETSNGNEQLLAVV 241
DB 181 AGEKMGTDDEEKFITIFGRSVSHLRKVPDKYMTISGFOEETIDETSNGNEQLLAVV 240
QY 242 KSIRSIPIALAEITLYYAMKAGAGTDHLLIRWVSRSEIDLFINIRKFRKNPATSLYSMTK 301
DB 241 KSIRSIPIALAEITLYYAMKAGAGTDHLLIRWVSRSEIDLFINIRKFRKNPATSLYSMTK 300
QY 302 GDTSGDYKALLLLCGEDD 320
DB 301 GDTSGDYKALLLLCGEDD 319

RESULT 12
ID ABG32550 standard; protein; 319 AA.
XX ABG32550;
XX 29-NOV-2002 (first entry)
XX Human CPB-1 protein.
XX

Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
 calcium/phospholipid binding protein; polyhydric alcohol.

Human sapiens.
 WO200267977-A1.

06-SEP-2002.

21-FEB-2002; 2002WO-0P001563.

26-FEB-2001; 2001JP-00050297.

(KOMA) KOMA CO LTD.
 (KAGA) CHERO-SERO-THERAPEUTIC RES INST.

Naruse H, Sano M, Shinoda Y, Inagi T;
 WPI; 2002-674988/72.

Eye drops for treating e.g. corneal diseases, contain CPB-I and
 polyhydric alcohol with specific carbonyl value, without unpleasant
 irritation upon dropping but with satisfactory long-term storability.

Disclosure; Page 13-14; 16pp; Japanese.

The invention relates to eye drops contain CPB-I (anexin V) and a
 polyhydric alcohol having a carbonyl value of not more than 50
 Mol.%. The eye drops are for treating e.g. corneal diseases. Such eye
 drops are without unpleasant irritation upon dropping but with
 satisfactory long-term storage stability. The present sequence is the
 human CPB-I (calcium/phospholipid binding) protein

Sequence 319 AA;

Query Match 99.7%; Score 1595; DB 5; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AQLVRLGVTDPGPPDERADAEFLTKRAMKGLGDESSITLTLTSSNAOROEISAAFKTLF 61
 Db 1 AQLVRLGVTDPGPPDERADAEFLTKRAMKGLGDESSITLTLTSSNAOROEISAAFKTLF 60

QY 62 GRDLDDDKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPEE 121
 Db 61 GRDLDDDKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPEE 120

QY 122 LRAIKQVEEYEGSSLEDVVDGTSYQYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 181
 Db 121 LRAIKQVEEYEGSSLEDVVDGTSYQYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 180

QY 182 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETTIRETSQNI 304LLAVV 241
 Db 181 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETTIRETSQNI 304LLAVV 240

QY 242 KSIRSIPAYLAETLYYAMKAGTDHTLIRVAVSSSEIDLFNIRKFRFNFAISLSYMTK 301
 Db 241 KSIRSIPAYLAETLYYAMKAGTDHTLIRVAVSSSEIDLFNIRKFRFNFAISLSYMTK 300

QY 302 GDTSGDYKAKALLLCGEDD 320
 Db 301 GDTSGDYKAKALLLCGEDD 319

RESULT 13
 ADE55088
 ID ADE55088 standard; protein; 319 AA.
 AC ADE55088;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P08758, SEQ ID NO 893.

Human; pain; neuronal tissue; gene therapy;
 spinal segmental nerve injury; chronic constriction injury; CCI;
 spared nerve injury; SNJ; Chung.

Human sapiens.
 WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-033347P.

(GENO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.

Wolff C, D'urso D, Befort K, Costigan M;
 WPI; 2003-268312/26.
 DR GENBANK; P08758.

New composition comprising two or more isolated polypeptides, useful for
 preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
 or human polynucleotides or a polynucleotide which represents a fragment,
 derivative or allelic variation of the nucleic acid sequence. Also
 claimed are a vector comprising the novel polynucleotide, a host cell
 comprising the vector, a method for identifying a nucleotide sequence
 which is differentially regulated in an animal subjected to pain and a
 kit to perform the method, an array, a method for identifying an agent
 that increases or decreases the expression of the polynucleotide sequence
 that is differentially expressed in neuronal tissue of a first animal
 subjected to pain, a method for identifying a compound which regulates
 the expression of a polynucleotide sequence which is differentially
 expressed in an animal subjected to pain, a method for identifying a
 compound that regulates the activity of one or more of the
 polynucleotides, a method for producing a pharmaceutical composition, a
 method for identifying a compound or small molecule that regulates the
 activity in an animal of one or more of the polynucleotides given in the
 specification, a method for identifying a compound useful in treating
 pain and a pharmaceutical composition comprising the one or more
 polypeptides or their antibodies. The polynucleotide or the compound that
 modulates its activity is useful for preparing a medicament for treating
 pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 injury (CCI) and spared nerve injury (SNJ)) in an animal (e.g. gene
 therapy). The sequence presented is a human protein (shown in Table 2 of
 the specification) which is differentially expressed during pain. Note:
 The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic form directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

Sequence 319 AA;

Query Match 99.7%; Score 1595; DB 7; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AQLVRLGVTDPGPPDERADAEFLTKRAMKGLGDESSITLTLTSSNAOROEISAAFKTLF 61
 Db 1 AQLVRLGVTDPGPPDERADAEFLTKRAMKGLGDESSITLTLTSSNAOROEISAAFKTLF 60

QY 62 GRDLDDDKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPEE 121
 Db 61 GRDLDDDKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPEE 120

QY 122 LRAIKQVEEYEGSSLEDVVDGTSYQYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 181

Db 121 LRAIKQVIEEYSSLEDDVVDTSYGYQRMVLVLQANRPDAGIDEXQVODQAQALFQ 180
 QY 182 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIPRETSNGNEQLLAVV 241
 Db 181 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIPRETSNGNEQLLAVV 240
 QY 242 KSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMTK 301
 Db 241 KSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMTK 300
 QY 302 GDTSGDYKAKALLLCCGEDD 320
 Db 301 GDTSGDYKAKALLLCCGEDD 319

RESULT 14
 ADE56187
 ID ADE56187 standard; protein; 319 AA.
 AC ADE56187;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P08758, SEQ ID NO 2036.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SN1; Chung.
 OS Homo sapiens.
 XX
 PN W0203016475-A2.
 PD 27-FEB-2003.
 XX
 PE 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P08758.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX

The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound
 CC modulates its activity is useful for preparing a medicament for treat-
 CC ing pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table
 CC the specification) which is differentially expressed during pain. No
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WPI
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

Sequence 319 AA;
 SQ

Query Match 99.7%; Score 1595; DB 7; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 2 AOVLRGVTYDPPGDERADAEETLRKAMKGLGTDSESLITLTSSNORQISAFKTL
 Db 1 AOVLRGVTYDPPGDERADAEETLRKAMKGLGTDSESLITLTSSNORQISAFKTL
 QY 62 GRDLDDDLKSELTKGFEKLIVALKPRLYDAVELKHALKGAGTNEKVLTEIISRTPE
 Db 61 GRDLDDDLKSELTKGFEKLIVALKPRLYDAVELKHALKGAGTNEKVLTEIISRTPE
 QY 122 LRAIKQVIEEYSSLEDDVVDTSYGYQRMVLVLQANRPDAGIDEXQVODQAQALF
 Db 121 LRAIKQVIEEYSSLEDDVVDTSYGYQRMVLVLQANRPDAGIDEXQVODQAQALF
 QY 182 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIPRETSNGNEQLLAVV
 Db 181 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIPRETSNGNEQLLAVV
 QY 242 KSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMTK
 Db 241 KSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMTK
 QY 302 GDTSGDYKAKALLLCCGEDD 320
 Db 301 GDTSGDYKAKALLLCCGEDD 319

RESULT 15
 AAP80242
 ID AAP80242 standard; protein; 320 AA.
 AC AAP80242;
 DT 25-MAR-2003 (revised)
 DT 12-SEP-1990 (first entry)
 XX
 DE Sequence vascular anticoagulating protein (VAP) VAC-alpha (Asp22).
 XX
 KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activ
 KW antiinflammatory; phospholipase inhibitor.
 OS Homo sapiens.
 XX
 PN W08807576-A.
 PD 06-OCT-1988.
 XX
 PE 26-MAR-1988; 88MO-BE000266.
 XX
 PR 28-MAR-1987; 87DE-03710309.
 PR 28-MAR-1987; 87DE-03710364.
 PR 28-MAR-1987; 87DE-03710430.
 PR 04-NOV-1987; 87DE-03737367.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Hauptmann R, Maurerfogy I, Bodo G, Swetly P, Stralow C;
 PI Falkner E, Adole G, Reutlingsp CMP;
 XX

DR WPI, 1988-292861/41.
 DR N-PSDB; AAN80872.
 XX New vascular anti-coagulating proteins - useful as thrombin inhibitors,
 PT antiinflammatory agents, etc.
 PS Claim 41, Page 171-72, 183pp; German.
 XX The DNA is produced by determining the amino acid sequence of isolated
 CC and highly purified VAPs, constructing DNA probes on the basis of this
 CC sequence, using the probes to search through suitable cDNA libraries,
 CC isolating cDNA that hybridises with the probes, by inserting the cDNA
 CC into a suitable vector, and using the vector to transform a host
 CC organism. VAC-alpha has anticoagulant activity under certain conditions,
 CC but loses this activity in the event of severe bleeding. It acts by
 CC inhibiting conversion of factor X to factor Xa and conversion of
 CC prothrombin to thrombin. It is structurally related to lipocortin I
 CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
 CC has similar antiinflammatory and phospholipase inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 CC
 CC Sequence 320 AA:
 XX
 SQ
 Query Match 99.6%; Score 1594; DB 1; Length 320;
 Best Local Similarity 99.4%; Pred. No. 4.6e-134;
 Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPFGFDERADAETLRKMKGLGTDEESILTLTSSRNAQROEISAARFRL 60
 DB 1 MAQVLRGTVDPFGFDERADAETLRKMKGLGTDEESILTLTSSRNAQROEISAARFRL 60
 QY 61 FGRDLDDLKSELTKSEKELIVALKMPSRLYDAVELKALKAGAGTNEKVLTEITASRPE 120
 DB 61 FGRDLDDLKSELTKSEKELIVALKMPSRLYDAVELKALKAGAGTNEKVLTEITASRPE 120
 QY 121 ELRAIKQYEEYEGSSLEDDVVGDTSGYQRMVLVLLQANDPDAGIDEAEOVDQAQLF 180
 DB 121 ELRAIKQYEEYEGSSLEDDVVGDTSGYQRMVLVLLQANDPDAGIDEAEOVDQAQLF 180
 QY 181 QAGELKMGTDDEKFTTIGTSSVSHLRKVPKMYTISGFOIEETDRETSQNLBOLLIAV 240
 DB 181 QAGELKMGTDDEKFTTIGTSSVSHLRKVPKMYTISGFOIEETDRETSQNLBOLLIAV 240
 QY 241 VKSIRSIPIAYLAETLYAMKAGAGTDDHTLIRVWVSRSSEIDLFNKKERRKQFATSLYSMI 300
 DB 241 VKSIRSIPIAYLAETLYAMKAGAGTDDHTLIRVWVSRSSEIDLFNKKERRKQFATSLYSMI 300
 QY 301 KGDTSQDYKALLLGCEDD 320
 DB 301 KGDTSQDYKALLLGCEDD 320

RESULT 16
 AAP80714
 ID AAP80714 standard; protein; 320 AA.
 XX AAP80714;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-SEP-1990 (first entry)
 XX
 DE Sequence vascular anticoagulating protein (VAP) VAC-alpha (Glu22).
 XX
 KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
 KW antiinflammatory; phospholipase inhibitory.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 7..18
 FT Peptide /label= tryptic peptide P18
 FT Peptide 30..45

FT Peptide /label= tryptic peptide P29/I
 FT Peptide 51..58
 FT Peptide /label= tryptic peptide P14
 FT Peptide 59..63
 FT Peptide /label= tryptic peptide P15
 FT Peptide 64..79
 FT Peptide /label= tryptic peptide P27
 FT Peptide 80..86
 FT Peptide /label= tryptic peptide P20/I
 FT Peptide 86..113
 FT Peptide /label= BRCN-peptide BRCN15
 FT Peptide 90..97
 FT Peptide /label= tryptic peptide P16/I
 FT Peptide 98..101
 FT Peptide /label= tryptic peptide P5
 FT Peptide 109..117
 FT Peptide /label= tryptic peptide P17
 FT Peptide 118..123
 FT Peptide /label= tryptic peptide P11/I
 FT Peptide 127..151
 FT Peptide /label= tryptic peptide P20/I
 FT Peptide 187..193
 FT Peptide /label= tryptic peptide P11/I
 FT Peptide 194..201
 FT Peptide /label= tryptic peptide P23/I
 FT Peptide 260..271
 FT Peptide /label= BRCN-peptide BRCN1
 FT Peptide 261..271
 FT Peptide /label= tryptic peptide P12
 FT Peptide 277..286
 FT Peptide /label= tryptic peptide P21
 FT Peptide 292..300
 FT Peptide /label= tryptic peptide P24
 FT Peptide 300..311
 FT Peptide /label= BRCN-peptide BRCN4

WO8807576-A.
 06-OCT-1988.
 XX
 XX 26-MAR-1988; 88WO-EP000266.
 XX 28-MAR-1987; 87DE-03710309.
 XX 28-MAR-1987; 87DE-03710364.
 XX 28-MAR-1987; 87DE-03710430.
 XX 04-NOV-1987; 87DE-03737367.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Hauptmann R, Maurerfogel I, Bodo G, Swetly P, Stratowa C;
 XX Falkner E, Adole G, Reutlingsp CMP;
 XX
 DR WPI, 1988-292861/41.
 DR N-PSDB; AAN80801.
 XX New vascular anti-coagulating proteins - useful as thrombin inhibitors,
 PT antiinflammatory agents, etc.
 PS Claim 41, Page 171 and Fig 4/1-4/2 and Fig 5/1-5/2, 183pp; German.
 XX The DNA is produced by determining the amino acid sequence of isolated
 CC and highly purified VAPs, constructing DNA probes on the basis of this
 CC sequence, using the probes to search through suitable cDNA libraries,
 CC isolating cDNA that hybridises with the probes, by inserting the cDNA
 CC into a suitable vector, and using the vector to transform a host
 CC organism. The poem. of the AA sequences used to construct the probes are
 CC given in FT. VAC-alpha has anticoagulant activity under certain
 CC conditions, but loses this activity in the event of severe bleeding. It
 CC acts by inhibiting conversion of factor X to factor Xa and conversion of
 CC prothrombin to thrombin. It is structurally related to lipocortin I
 CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
 CC has similar antiinflammatory and phospholipase inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to

CC correct PA field.)
XX
SQ Sequence 320 AA;

Query Match 99.6%; Score 1594; DB 1; Length 320;
Best Local Similarity 99.4%; Pred. No. 4.6e-134;
Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLKGVTPDPGPDERRADAETLRKAMKGLGTDSESLITLTSNSNAQROEISAFAKTL 60
DB 1 MAQVLKGVTPDPGPDERRADAETLRKAMKGLGTDSESLITLTSNSNAQROEISAFAKTL 60
QY 61 FGRDLDDLKSELTKGKEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
DB 61 FGRDLDDLKSELTKGKEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
QY 121 ELRAIKQVVEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDAQALF 180
DB 121 ELRAIKQVVEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDAQALF 180
QY 181 QAGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
DB 181 QAGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
QY 241 VKSIRSIPIAYLAETLYYAMKAGAGTDHTLIRWVSRSEIDLFNIRKEFRKNFATSLYSMT 300
DB 241 VKSIRSIPIAYLAETLYYAMKAGAGTDHTLIRWVSRSEIDLFNIRKEFRKNFATSLYSMT 300
QY 301 KGDTSGDYKALLLLCGEDD 320
DB 301 KGDTSGDYKALLLLCGEDD 320

RESULT 17

AAR11910
ID AAR11910 standard; protein, 320 AA.

XX AAR11910;

DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 25-JUL-1991 (first entry)

XX Vascular anticoagulant protein.

XX Annexin; anticoagulant; tumour metastasis; fibrin; cancer.

OS Homo sapiens.

PH Key Location/Qualifiers
FT Misc_difference 22..22
FT /label= Glu, Asp

XX DE3937607-A.

XX 16-MAY-1991.

XX 11-NOV-1989; 89DE-03937607.

XX 11-NOV-1989; 89DE-03937607.

XX (BOEH) BOEHRINGER INGELHEIM.

XX Reutelings CP;

XX WPI; 1991-149572/21.

PT Anticoagulants contg. annexin or its analogues and derivs. - used to
PT treat tumours and to reduce metastases.

XX Claim 3; Page 11; 17pp; German.

XX This vascular anticoagulant protein (VAC) comprises an annexin. It is

CC formulated with auxiliaries, carriers and/or stabilisers for prevent
CC tumour cell metastasis. Admin. is by injection, in a pref. dosage of
CC -0.05 mg/Kg, or using a topical formulation in a dosage of 0.25-10 m
CC ml soln. or 10g gel. (Updated on 10-MAR-2003 to add missing OS field
CC (updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 320 AA;

Query Match 99.6%; Score 1594; DB 2; Length 320;
Best Local Similarity 99.7%; Pred. No. 4.6e-134;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLKGVTPDPGPDERRADAETLRKAMKGLGTDSESLITLTSNSNAQROEISAFAKTL 60
DB 1 MAQVLKGVTPDPGPDERRADAETLRKAMKGLGTDSESLITLTSNSNAQROEISAFAKTL 60
QY 61 FGRDLDDLKSELTKGKEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
DB 61 FGRDLDDLKSELTKGKEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
QY 121 ELRAIKQVVEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDAQALF 180
DB 121 ELRAIKQVVEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDAQALF 180
QY 181 QAGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
DB 181 QAGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
QY 241 VKSIRSIPIAYLAETLYYAMKAGAGTDHTLIRWVSRSEIDLFNIRKEFRKNFATSLYSMT 300
DB 241 VKSIRSIPIAYLAETLYYAMKAGAGTDHTLIRWVSRSEIDLFNIRKEFRKNFATSLYSMT 300
QY 301 KGDTSGDYKALLLLCGEDD 320
DB 301 KGDTSGDYKALLLLCGEDD 320

RESULT 18

AAR26180
ID AAR26180 standard; protein, 319 AA.

XX AAR26180;

DT 10-MAR-2003 (revised)
DT 04-FEB-1993 (first entry)

XX CPB-1.

XX CPB-1; saccharides; stabilisation; antihemagglutination; dermal disea
XX corneal disease.

OS Homo sapiens.

XX JP04198196-A.

XX 17-JUL-1992.

XX 28-NOV-1990; 90JP-00328287.

XX 28-NOV-1990; 90JP-00328287.

XX (KOMA) KOMA CO LTD.
XX (KAGA) KAGAKU OYOH KESSEI RYOHO.

XX WPI; 1992-288938/35.

PT Stabilisation of CPB-1 for drug compsn. - contains saccharide selected
PT from glucose, glucosamine, xylose, saccharose and/or dextran.

XX Disclosure; Page 2; 4pp; Japanese.

XX The sequence given is the amino acid sequence of CPB-1. CPB-1 was used
XX within the method of the invention which involved adding saccharides t

it which resulted in its stabilisation. The saccharide was pref. glucose, glucosamine, xylose, saccharose, or dextran. This lead to the production of CPB-I which kept its activity when it had been processed by several treatments. CPB-1 can be used as a medicine for antiemagglutination, CC demal and corneal diseases. (updated on 10-MAR-2003 to add missing OS field.)

CC Sequence 319 AA;

Query Match 99.4%; Score 1590; DB 2; Length 319;
Best Local Similarity 99.7%; Pred. No. 1e-133;
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQLVKGTVTDFFGFERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTLF 61
DB 1 AQLVKGTVTDFFGFERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTLF 60
QY 62 GRDLDDDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGNEKVLTEIIASRTPE 121
DB 61 GRDLDDDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGNEKVLTEIIASRTPE 120
QY 122 LPAIKQVVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQ 181
DB 121 LPAIKQVVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQ 180
QY 182 AGEKMGCTDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEJLLAV 241
DB 181 AGEKMGCTDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEJLLAV 240
QY 242 KSIKRSIPAYIAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKEPRKNFATSLYSMT 301
DB 241 KSIKRSIPAYIAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKEPRKNFATSLYSMT 300
QY 302 GDTSGDYKALLLLCGEDD 320
DB 301 GDTSGDYKALLLLCGEDD 319

RESULT 19

AAB50864 standard; protein; 327 AA.

XX AAB50864;
AC 16-MAR-2001 (first entry)
DT Modified human annexin, SEQ ID NO: 4.
DE Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplamt rejection.
XX Homo sapiens.
OS WO200073332-A1.
PN 07-DEC-2000.
PD 25-MAY-2000; 2000WO-US014324.
PF 01-JUN-1999; 99US-00324096.
PR (UNITW) UNIV WASHINGTON.
PA Tait JF, Brown DS;
XX WPI, 2001-080465/09.
DR N-PSDB; AAC91369.
XX Novel modified annexin useful for imaging vascular thrombi and apoptosis,
PT has N-terminal chelation site comprising amino acid extension which
PS comprises a glycine and a cysteine residue.
Claim 15; Page 33-35; 39pp; English.

XX The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bioactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity

CC Sequence 327 AA;

Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 1e-133;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQLVKGTVTDFFGFERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTL 60
DB 8 MAQLVKGTVTDFFGFERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTL 67
QY 61 FGRDLDDDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGNEKVLTEIIASRTPE 120
DB 68 FGRDLDDDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGNEKVLTEIIASRTPE 127
QY 121 ELPAIKQVVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALF 180
DB 128 ELPAIKQVVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALF 187
QY 181 AGEKMGCTDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEJLLAV 240
DB 188 AGEKMGCTDEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEJLLAV 247
QY 241 VKSIRSIPIAYIAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKEPRKNFATSLYSMT 300
DB 248 VKSIRSIPIAYIAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKEPRKNFATSLYSMT 307
QY 301 KQDTSGDYKALLLLCGEDD 320
DB 308 KQDTSGDYKALLLLCGEDD 327

RESULT 20

AAB50865 standard; protein; 327 AA.

XX AAB50865;
AC 16-MAR-2001 (first entry)
DT Modified human annexin, SEQ ID NO: 6.
DE Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplamt rejection.
XX Homo sapiens.
OS WO200073332-A1.
PN 07-DEC-2000.
PD 25-MAY-2000; 2000WO-US014324.
PF 01-JUN-1999; 99US-00324096.
PR (UNITW) UNIV WASHINGTON.
PA Tait JF, Brown DS;
XX WPI, 2001-080465/09.
DR N-PSDB; AAC91370.

XX Novel modified annexin useful for imaging vascular thrombi and apoptosis,
PT has N-terminal chelation site comprising amino acid extension which
XX comprises a glycine and a cysteine residue.

PS Claim 18; Page 37-38; 39pp; English.

XX The present sequence is a modified annexin having an N-terminal chelation
CC site, which comprises an amino acid extension including a glycine and a
CC cysteine residue. The modified annexin is useful for imaging vascular
CC thrombi or apoptosis which is associated with response to a
CC chemotherapeutic agent or with rejection as a result of transplantation.
CC The modified annexin can effectively chelate a radionuclide and retain
CC annexin bioactivity. It can be readily prepared in high radiochemical
CC yield and with high radiochemical purity. In contrast to conventional
CC conjugation chemistries that provide a distribution of conjugation
CC products, the modified annexin has a single chelation site remote from
CC the site of biological activity

SQ Sequence 327 AA;

Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.1e-133;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDTPGPDERRADAEFLRKAMKGLGDEESITLTLSRNAQROEISAAPKTL 60
DB 8 MAQVLRGTVDTPGPDERRADAEFLRKAMKGLGDEESITLTLSRNAQROEISAAPKTL 67
QY 61 FGRLDLDLKSLETKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIISRTPE 120
DB 68 FGRLDLDLKSLETKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIISRTPE 127
QY 121 ELRAIKQVYEEYSGSLDDVDVGTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
DB 128 ELRAIKQVYEEYSGSLDDVDVGTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 187
QY 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQILLAV 240
DB 188 QAGELKMGTDDEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQILLAV 247
QY 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFRKNPATSLYSMTI 300
DB 248 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFRKNPATSLYSMTI 307
QY 301 KGDTSGDYKKALLLLCGEDD 320
DB 308 KGDTSGDYKKALLLLCGEDD 327

RESULT 21

AAB50863 ID AAB50863 standard; protein; 327 AA.

AC AAB50863;

DT 16-MAR-2001 (first entry)

DE Modified human annexin, SEQ ID NO: 2.

KW Human; annexin; chelation site; nuclear imaging; apoptosis;
transplant rejection.

OS Homo sapiens.

PN MO200073332-A1.

PD 07-DEC-2000.

PF 25-MAY-2000; 2000MO-US014324.

PR 01-JUN-1999; 99US-00324096.

XX

PA (UNITV) UNIV WASHINGTON.

XX Tait JF, Brown DS;

DR WPI; 2001-080465/09.

DR N-PSDB; AAC91368.

PT Novel modified annexin useful for imaging vascular thrombi and apopt
PT has N-terminal chelation site comprising amino acid extension which
XX comprises a glycine and a cysteine residue.

PS Claim 12; Page 30-31; 39pp; English.

XX The present sequence is a modified annexin having an N-terminal chel
CC site, which comprises an amino acid extension including a glycine an
CC cysteine residue. The modified annexin is useful for imaging vascula
CC thrombi or apoptosis which is associated with response to a
CC chemotherapeutic agent or with rejection as a result of transplanat
CC The modified annexin can effectively chelate a radionuclide and reta
CC annexin bioactivity. It can be readily prepared in high radiochemica
CC yield and with high radiochemical purity. In contrast to conventiona
CC conjugation chemistries that provide a distribution of conjugation
CC products, the modified annexin has a single chelation site remote fr
CC the site of biological activity

SQ Sequence 327 AA;

Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.1e-133;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDTPGPDERRADAEFLRKAMKGLGDEESITLTLSRNAQROEISAAPKTL 120
DB 8 MAQVLRGTVDTPGPDERRADAEFLRKAMKGLGDEESITLTLSRNAQROEISAAPKTL 127
QY 61 FGRLDLDLKSLETKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIISRTPE 240
DB 68 FGRLDLDLKSLETKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIISRTPE 247
QY 121 ELRAIKQVYEEYSGSLDDVDVGTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 300
DB 128 ELRAIKQVYEEYSGSLDDVDVGTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 307
QY 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQILLAV 320
DB 188 QAGELKMGTDDEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQILLAV 327
QY 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFRKNPATSLYSMTI 320
DB 248 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFRKNPATSLYSMTI 327
QY 301 KGDTSGDYKKALLLLCGEDD 320
DB 308 KGDTSGDYKKALLLLCGEDD 327

RESULT 22

AAP91363 ID AAP91363 standard; protein; 320 AA.

AC AAP91363;

DT 22-DEC-1989 (first entry)

DE Human lipocortin-V.

KW Human lipocortin-V; lambdaBHLipo V-1; anti-inflammatory agent.

OS Homo sapiens.

PN EP30396-A.

PD 30-AUG-1989.

XX

XX 20-FEB-1989, 89EP-00301603.
 XX 26-FEB-1988, 88US-00160866.
 XX (BIOI) BIOGEN INC.
 XX (BIOI) BIOGEN INC.
 XX Wallner BP, Pepinsky RB, Browning JL;
 PI WPI, 1989-250486/35.
 XX Human lipocortin cpds. III, IV, V, and VI - used in treatment of
 PT arthritic, allergic, dermatologic, ophthalmic and collagen disorders
 PT involving inflammatory processes.
 XX Claim 16, Fig 4, 32pp; English.
 XX Human lipocortin-V was isolated from a lambda gt10 human peripheral blood
 CC lymphocyte cDNA library with rat lipocortin-V cDNA of lambda Riipo V-1 as
 CC probe. Lipocortins are anti-inflammatory agents and can be used to treat
 CC arthritic, allergic, dermatologic, ophthalmic, and collagen diseases. See
 CC also AAN90598, AAN90599, and AAP91362
 XX

Sequence 320 AA;
 Query Match 99.2%; Score 1587; DB 1; Length 320;
 Best Local Similarity 99.4%; Pred. No. 1.9e-133;
 Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNOVLRGVTDPFGFDERADAEITLRKAMKGLTDEESITLTLSRSNAQROEISAFAKTL 60
 DB 1 MNOVLRGVTDPFGFDERADAEITLRKAMKGLTDEESITLTLSRSNAQROEISAFAKTL 60
 QY 61 FGRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 120
 DB 61 FGRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 181 QAGELKMGTEDEKFTITFGTRSVSHLRKVDKMTISGFOIETIDETSNGLEQLLAV 240
 DB 181 QAGELKMGTEDEKFTITFGTRSVSHLRKVDKMTISGFOIETIDETSNGLEQLLAV 240
 QY 181 QAGELKMGTEDEKFTITFGTRSVSHLRKVDKMTISGFOIETIDETSNGLEQLLAV 240
 DB 181 QAGELKMGTEDEKFTITFGTRSVSHLRKVDKMTISGFOIETIDETSNGLEQLLAV 240
 QY 241 VKSIRSIPIALAEITLYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300
 DB 241 VKSIRSIPIALAEITLYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 23

AAR25718 standard; protein, 319 AA.

XX AAR25718;
 XX 18-JAN-1993 (first entry)
 XX CPB-1.
 XX Nerve cell protecting agent; placenta.
 XX Homo sapiens.
 XX JP04173744-A.
 XX 22-JUN-1992.
 XX

PF 02-NOV-1990; 90JP-00298036.
 XX 02-NOV-1990; 90JP-00298036.
 XX (KOMA) KOMA CO LTD.
 XX WPI, 1992-255655/31.
 XX Use of human placenta derived coagulation inhibitor, CPB-1 - for
 PT preventing and treating senile dementia and brain vessel lesions.
 XX Disclosure; Page 3; 5pp; Japanese.
 XX The sequence given is a nerve cell protecting agent containing human CPB-
 CC 1. The CPB-1 acts as a growth nutrition factor for nerve cells and the
 CC agent containing it is useful for the prevention and treatment of various
 CC diseases such as senile dementia and brain vessel lesions. The current
 CC agent is derived from human placenta and are free of side effects and
 CC are harmless to the living body
 XX

Sequence 319 AA;
 Query Match 97.7%; Score 1563; DB 2; Length 319;
 Best Local Similarity 98.7%; Pred. No. 2.7e-131;
 Matches 315; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AOVLRGVTDPFGFDERADAEITLRKAMKGLTDEESITLTLSRSNAQROEISAFAKTL 61
 DB 1 AOVLRGVTDPFGFDERADAEITLRKAMKGLTDEESITLTLSRSNAQROEISAFAKTL 60
 QY 62 GRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 121
 DB 61 GRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 122 LRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 181
 DB 121 LRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
 QY 121 LRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
 DB 121 LRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
 QY 182 AGELKMGTEDEKFTITFGTRSVSHLRKVDKMTISGFOIETIDETSNGLEQLLAV 241
 DB 181 AGELKMGTEDEKFTITFGTRSVSHLRKVDKMTISGFOIETIDETSNGLEQLLAV 240
 QY 242 KSIIRSIPIALAEITLYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 301
 DB 241 KSIIRSIPIALAEITLYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300
 QY 302 GDTSGDYKKALLLLCGEDD 320
 DB 301 GDTSGDYKKALLLLCGEDD 319

RESULT 24

AA113924 standard; protein, 319 AA.

XX AA113924;
 XX 13-JUL-1999 (first entry)
 XX S65T GFP variant/hannexin V protein.
 XX GFP, green fluorescent protein; annexin; fusion protein; apoptosis;
 KW fluorescent intensity; anionic phospholipid binding affinity;
 KW asymmetric distribution; plasma membrane phospholipid;
 KW apoptotic cell detection.
 XX Aequorea victoria.
 XX Homo sapiens.
 XX Synthetic.
 XX WO9919470-A2.
 XX 22-APR-1999.
 XX

XX 09-OCT-1998; 98WO-US021444.
 XX 09-OCT-1997; 97US-00948276.
 PR (REGC) UNIV CALIFORNIA.
 PA
 XX Ernst JD;
 XX WPI; 1999-277634/23.
 DR
 XX Bifunctional fusion protein useful for the detection of apoptotic cells.
 PT
 XX Claim 2; Page 15-17; 23pp; English.
 PS
 XX This sequence represents an example of a protein of the invention. The
 CC proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labeled annexin, with
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes
 XX
 SQ Sequence 319 AA;
 Query Match 93.0%; Score 1488.5; DB 2; Length 319;
 Best Local Similarity 94.0%; Pred. No. 1.2e-124;
 Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 6 RGVTTDPGDEADAEATLRKAMKGLGTDEESITLTLSRSNAQROEISAFAKTLFGKRL 65
 DB 4 RGVTTDPGDEADAEATLRKAMKGLGTDEESITLTLSRSNAQROEISAFAKTLFGKRL 63
 QY 66 LDDLKSELTKFEKLIYALMKPSRLYAYELKALKAGAGNEKVLTEIIASRPEELRAI 125
 DB 64 VDDLKSELTKFEKLIYAMMKPSRLYAYELKALKAGAGNEKVLTEIIASRPEELSAI 123
 QY 126 KQYEEYEGSSLEDVVDGTSYGQRMVVLQANRPDPAGIDEAQVEQDAQALFOAGEL 185
 DB 124 KQYEEYEGSSLEDVVDGTSYGQRMVVLQANRPDPAGIDEAQVEQDAQALFOAGEL 183
 QY 186 KMGTEDEKFTITIGTSVSHLRKVPDKYMTISGFOIETIDRETSNGLLEQLLAAVKSIR 245
 DB 184 KMGTEDEKFTITIGTSVSHLRKVPDKYMTISGFOIETIDRETSNGLLEQLLAAVKSIR 243
 QY 246 SIPAYLAETLYYAMKAGATDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMIKGDTS 305
 DB 244 SIPAYLAETLYYAMKAGATDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMIKGDTS 303
 QY 306 GDYKKALLLILC-GEED 320
 DB 304 GDYKKALLLILC-GEED 319

RESULT 25
 ABB57067
 ID ABB57067 standard; protein; 319 AA.
 XX ABB57067;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:136.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 XX Mus musculus.
 OS
 XX WO20018188-A2.
 EN
 XX
 XX 22-NOV-2001.
 PD
 XX 18-MAY-2001; 2001WO-JP004192.
 PF
 XX 18-MAY-2000; 2000JP-00145977.
 PR
 XX (UNVI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 PA
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 PI WPI; 2002-034733/04.
 DR N-PSDB; AB199289.
 XX
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measur
 PT expression levels of particular genes defined in the specification o
 PT determining the expression profile of a gene group comprising these
 PT genes.
 PS
 XX Claim 2; Page 419-421; 2690pp; English.
 PS
 XX The present invention describes a method for examining ischemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of
 CC a gene group in the sample comprising genes selected from (I). The met
 CC is useful for examining the ischemic condition (e.g. compressive
 CC ischemia, occlusive ischemia or vasospastic ischemia) by measurin
 CC expression levels of particular genes (AB199202 to AB199912, encodin
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expre
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutic for ischaemic diseases. AB199913 and AB199914 represent
 CC primers for a mouse ischaemic condition related sequence, which are
 CC in the exemplification of the present invention
 CC
 XX
 SQ Sequence 319 AA;
 Query Match 93.0%; Score 1488.5; DB 5; Length 319;
 Best Local Similarity 94.0%; Pred. No. 1.2e-124;
 Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 6 RGVTTDPGDEADAEATLRKAMKGLGTDEESITLTLSRSNAQROEISAFAKTLFGKRL 65
 DB 4 RGVTTDPGDEADAEATLRKAMKGLGTDEESITLTLSRSNAQROEISAFAKTLFGKRL 63
 QY 66 LDDLKSELTKFEKLIYALMKPSRLYAYELKALKAGAGNEKVLTEIIASRPEELRAI 125
 DB 64 VDDLKSELTKFEKLIYAMMKPSRLYAYELKALKAGAGNEKVLTEIIASRPEELSAI 123
 QY 126 KQYEEYEGSSLEDVVDGTSYGQRMVVLQANRPDPAGIDEAQVEQDAQALFOAGEL 185
 DB 124 KQYEEYEGSSLEDVVDGTSYGQRMVVLQANRPDPAGIDEAQVEQDAQALFOAGEL 183
 QY 186 KMGTEDEKFTITIGTSVSHLRKVPDKYMTISGFOIETIDRETSNGLLEQLLAAVKSIR 245
 DB 184 KMGTEDEKFTITIGTSVSHLRKVPDKYMTISGFOIETIDRETSNGLLEQLLAAVKSIR 243
 QY 246 SIPAYLAETLYYAMKAGATDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMIKGDTS 305
 DB 244 SIPAYLAETLYYAMKAGATDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMIKGDTS 303
 QY 306 GDYKKALLLILC-GEED 320
 DB 304 GDYKKALLLILC-GEED 319

Search completed: March 25, 2004, 08:04:54

ANX5 HUMAN
ID ANX5 HUMAN STANDARD; PRT; 319 AA.
AC P08758;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-1) (Placental anticoagulant protein I) (PAP-1) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchoring C11).
GN ANX5 OR ANX5 OR ENX2 OR PP4.
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86234495; PubMed=2967495;
RA Grundmann U., Abel K.-J., Bohn H., Loebermann H., Lottspeich F.,
RA Kuemper H.;
RT "Characterization of cDNA encoding human placental anticoagulant
RT protein (PP4): homology with the lipocortin family.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=86273329; PubMed=2455636;
RA Maurer-Fogy I., Reutelingersperger C.P.M., Pieters J., Bodo G.,
RA Stratowa C., Hauptmann R.;
RT "Cloning and expression of cDNA for human vascular anticoagulant, a
RT Ca2+-dependent phospholipid-binding protein.";
RL Eur. J. Biochem. 174:585-592(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86273202; PubMed=2968983;
RA Pepinsky R.B., Tizard R., Mateliano R.J., Sinclair L.K., Miller G.T.,
RA Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter L.,
RA Hession C., Frey A.Z., Wallner B.P.;
RT "Five distinct calcium and phospholipid binding proteins share
RT homology with lipocortin I.";
RL J. Biol. Chem. 263:10799-10811(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=86163463; PubMed=2964863;
RA Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;
RL Biochemistry 26:8087-8092(1987).
RN [5]
RP SEQUENCE FROM N.A., AND SEQUENCE.
RX MEDLINE=86139278; PubMed=2963810;
RA Iwasaki A., Suda M., Nakao H., Nagoya T., Saino Y., Arai K.,
RA Mizoguchi T., Sato F., Yoshizaki H., Hirata M., Miyata T.,
RA Shitara Y., Murata M., Maki M.;
RT "Structure and expression of cDNA for an inhibitor of blood
RT coagulation isolated from human placenta: a new lipocortin-like
RT protein.";
RL J. Biochem. 102:1261-1273(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=86228020; PubMed=2967291;
RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
RT "Cloning and expression of cDNA for human endonexin II, a Ca2+ and
RT phospholipid binding protein.";
RL J. Biol. Chem. 263:8037-8043(1988).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
MEDLINE=95047484; PubMed=7958998;
RA Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
RT "The gene encoding human annexin V has a TATA-less promoter with a
RT high G+C content.";
RL Gene 149:253-260(1994).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94307733; PubMed=8034319;
RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
RA Tait J.F.;
RT "Organization of the human annexin V (ANX5) gene.";
RL Genomics 20:463-467(1994).
RN [9]
RP SEQUENCE FROM N.A.
RX TISSUE=Muscle, Ovary, and Skin;
MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carinci P., Mullaly S.J.,
RA Raka S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=90088443; PubMed=2532007;
RA Rochhut R., Comera C., Cortial S., Haumont P.-Y., Diep Le K.H.,
RA Cavado J.C., Conard J., Russo-Marie F., Lederer F.;
RT "A 32 kDa lipocortin from human mononuclear cells appears to be
RT identical with the placental inhibitor of blood coagulation.";
RL Biochem. J. 263:929-935(1989).
RN [11]
RP SEQUENCE OF 85-130, 258-296 AND 299-319.
RX MEDLINE=87317598; PubMed=2957692;
RA Schlaepfer D.D., Mehlman T., Burgess W.H., Haigler H.T.;
RT "Structural and functional characterization of endonexin II, a
RT calcium and phospholipid-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
RN [12]
RP SEQUENCE OF 84-92.
RX MEDLINE=89066552; PubMed=2974032;
RA Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
RA de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
RT phospholipase A2 inhibitors from human placenta. Evidence against a
RT mechanistically relevant association between enzyme and inhibitor.";
RL J. Biol. Chem. 263:18657-18663(1988).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=91065314; PubMed=2147412;
RA Huber R., Roemisch J., Paques E.-P.;
RT "The crystal and molecular structure of human annexin V, an
RT anticoagulant protein that binds to calcium and membranes.";
RL EMBO J. 9:3867-3874(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91085549; PubMed=2148156;
RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
RT "The calcium binding sites in human annexin V by crystal structure
RT analysis at 2.0-A resolution. Implications for membrane binding and
RT calcium channel activity.";
RL FEBS Lett. 275:15-21(1990).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92177413; PubMed=1311770;
RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
RA Luecke H., Roemisch J., Paques E.-P.;

RT "Crystal and molecular structure of human annexin V after refinement.
 RT implications for structure, membrane binding and ion channel
 RT formation of the annexin family of proteins.";
 RL J. Mol. Biol. 223:683-704(1992).
 RN [16]
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RP MEDLINE=98062349; PubMed=9398511;
 RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
 RA "Crystal structure of annexin V with its ligand K-201 as a calcium
 RT channel activity inhibitor";
 RL J. Mol. Biol. 274:16-20(1997).
 RN [17]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE=98118533; PubMed=9435213;
 RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
 RA "Residue-specific bioincorporation of non-natural, biologically
 RT active amino acids into proteins as possible drug carriers: structure
 RT and stability of the per-thioproline mutant of annexin V.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
 CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
 CC indirect inhibitor of the thromboplastin-specific complex, which
 CC is involved in the blood coagulation cascade.
 CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -1- CAUTION: This protein has been independently sequenced by at least
 CC seven groups under different names!
 CC -1- DATABASE: NAME=RED Systems' cytokine source book: Annexin 5;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=185".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X12454; CAJ30985.1; -;
 DR EMBL: M19384; AAB59545.1; -;
 DR EMBL: M18366; AAA35570.1; -;
 DR EMBL: M21731; AAA36166.1; -;
 DR EMBL: D00172; BAA00122.1; -;
 DR EMBL: U03745; AAA52386.1; -;
 DR EMBL: U01691; AAB40047.1; -;
 DR EMBL: U01681; AAB40047.1; JOINED.
 DR EMBL: U01682; AAB40047.1; JOINED.
 DR EMBL: U01683; AAB40047.1; JOINED.
 DR EMBL: U01685; AAB40047.1; JOINED.
 DR EMBL: U01686; AAB40047.1; JOINED.
 DR EMBL: U01687; AAB40047.1; JOINED.
 DR EMBL: U01689; AAB40047.1; JOINED.
 DR EMBL: U01690; AAB40047.1; JOINED.
 DR -----
 Query Match 99.7%; Score 1595; DB 1; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1.ee-96;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 AGELKMGTDSEKFTTIGTSVSHLRVFDKMTTISGFQIEETIDRETSGNLEQLLAVV
 QY 242 KSISIPVAYAEITYAMKAGTGDHILIRVWSRSEIDLFNIRKFRKNFATSLYSMT
 DB 241 KSISIPVAYAEITYAMKAGTGDHILIRVWSRSEIDLFNIRKFRKNFATSLYSMT
 QY 302 GDTSGDYKALLLCEGDD 320
 DB 301 GDTSGDYKALLLCEGDD 319
 RESULT 2
 ANX5_BOVIN STANDARD; PRT; 320 AA.
 AC P81287;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipoportin V) (Endonexin II) (Calphobindin I
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha
 DE (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93041974; PubMed=1420335;
 RA Learmonth M.P., Howell S.A., Harris A.C.M., Ames B., Patel Y.,
 RA Giannanco I., Bianchi R., Pala G., Ceccarelli P., Donato R.,
 RA Green B.N., Altken A.;
 RT "Novel isoforms of CaBP 33/37 (annexin V) from mammalian brain:
 RT structural and phosphorylation differences that suggest distinct
 RT biological roles.";
 RL Biochem. Biophys. Acta 1160:76-83(1992).
 CC -1- FUNCTION: This protein is an anticoagulant protein that acts as
 CC an indirect inhibitor of the thromboplastin-specific complex,
 CC which is involved in the blood coagulation cascade.
 CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 DR PIR: S27214; S27214.
 DR HSSP: P08758; 1ANW.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Acetylation.
 FT INTT MET 0 0
 FT REPEAT 23 83 ANNEXIN 1.
 FT REPEAT 95 155 ANNEXIN 2.
 FT REPEAT 179 239 ANNEXIN 3.
 FT REPEAT 254 314 ANNEXIN 4.
 FT MOD RES 1 1 ACETYLTATION (BY SIMILARITY).
 FT VARIANT 36 36 S -> T.
 FT VARIANT 125 125 K -> E.
 FT SEQUENCE 320 AA; 35942 MW; 50FCET8B95F19CB0 CRC64;
 Query Match 96.6%; Score 1545.5; DB 1; Length 320;
 Best Local Similarity 96.9%; Pred. No. 2.6e-93;
 Matches 310; Conservative 5; Mismatches 4; Indels 1; Gaps 0;
 QY 2 AQLVIGTVTDPGFERADAEFLRKAMKGLCTDEBSITLTLSNNAQROEISAAPKLF

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Db 1 AOVNRTVADFPGPDERADAEFLRKAMKGLGDEESILTLTSSNAQOEIAVAFKTLF 60
QY 62 GRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGNEKVLTEIIASRTPEE 121
Db 61 GRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGDEKVLTEIISRPTEE 120
QY 122 LRAIKQVEEYEGSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 181
Db 121 LRAIKQVEEYEGSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
QY 182 AGEKMGWDEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSGNLEQLLAVV 241
Db 181 AGEKMGWDEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSGNLEQLLAVV 240
QY 242 KSIRSIPIAYIAETLYAMKAGCTDHTLIRVMSRSEIDLFNIRKFRKPFATSLYSMTIK 301
Db 241 KSIRSIPIAYIAETLYAMKAGCTDHTLIRVMSRSEIDLFNIRKFRKPFATSLYSMTIK 300
QY 302 GDTSGDYKALLLLC-GEED 320
Db 301 GDTSGDYKALLLLC-GEED 320

```

RESULT 3

ANX5 MOUSE

ID ANX5 MOUSE STANDARD; PRT; 319 AA.

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AC P48036;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-1) (Placental anticoagulant protein I) (PAP-1) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchoirin CII)
DE ANXAS OR ANXS
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxId=10090;
RN [1]
RP TISSUE=Peritoneal cavity;
RP MEDLINE=96422179; PubMed=8824796;
RX Rodriguez-garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
RT "Mouse annexin V chromosomal localization, cDNA sequence
RT conservation, and molecular evolution.";
RT Genomics 31:151-157(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Adachi T., Kojima K., Fukuoaka S.-I., Ogawa H., Matsumoto I.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RC MEDLINE=99072820; PubMed=9854034;
RA Rodriguez-garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,
RA Fernandez M.P.;
RT "Mouse annexin V genomic organization includes an endogenous
RT retrovirus.";
RT J. Biochem. 337:125-131(1999).
CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplastin-specific complex, which
CC is involved in the blood coagulation cascade.
CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC DR EMBL; U29396; AAC52530.1; -
CC DR EMBL; D63423; BAA09728.1; -
CC DR EMBL; AJ230108; CA113092.1; -
CC DR EMBL; AJ230110; CA113092.1; JOINED.
CC DR EMBL; AJ230111; CA113092.1; JOINED.
CC DR EMBL; AJ230114; CA113092.1; JOINED.
CC DR EMBL; AJ230116; CA113092.1; JOINED.
CC DR EMBL; AJ230118; CA113092.1; JOINED.
CC DR EMBL; AJ230119; CA113092.1; JOINED.
CC DR EMBL; AJ230120; CA113092.1; JOINED.
CC DR EMBL; AJ230121; CA113092.1; JOINED.
CC DR EMBL; AJ230122; CA113092.1; JOINED.
CC DR EMBL; AJ230123; CA113092.1; JOINED.
CC DR EMBL; AJ230124; CA113092.1; JOINED.
CC DR HSSP; P14668; 1A8B.
CC DR SWISS-2DPAGE; P48036; MOUSE.
CC DR MGD; MGI:106008; Anx5.
CC DR InterPro; IPR001464; Annexin.
CC DR Pfam; PF00191; annexin; 4.
CC DR PRINTS; PR00196; ANNEXIN.
CC DR PRODOM; PD000143; ANNEXIN.
CC DR SMART; SM00335; ANX; 4.
CC DR PROSITE; PS00223; ANNEXIN; 4.
CC KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
CC KW Placenta.
CC FT REPEAT 22 82 ANNEXIN 1.
CC FT REPEAT 94 154 ANNEXIN 2.
CC FT REPEAT 178 238 ANNEXIN 3.
CC FT REPEAT 253 313 ANNEXIN 4.
CC SQ SEQUENCE 319 AA; 35752 MW; 55055BAF2E1C36B7 CRC64;

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Query Match 93.0%; Score 1488.5; DB 1; Length 319;
Best local Similarity 94.0%; Pred. No. 1.3e-89;
Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

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QY 6 RGVTDLPFGDERADAEFLRKAMKGLGDEESILTLTSSNAQOEISAARKTLFGRDL 65
Db 4 RGVTDLPFGDERADAEFLRKAMKGLGDEESILTLTSSNAQOEISAARKTLFGRDL 63
QY 66 LDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGNEKVLTEIIASRTPEELRAI 125
Db 64 VDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTDEKVLTEIIASRTPEELSAI 123
QY 126 KQVEEYEGSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 124 KQVEEYEGSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 183
QY 186 KWGDEEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSGNLEQLLAVVKSIR 245
Db 184 KWGDEEKFTITIGTRSVSHLRKVPDKYMTISGFOIETTIDRETSGNLEQLLAVVKSIR 243
QY 246 SIPAYIAETLYAMKAGCTDHTLIRVMSRSEIDLFNIRKFRKPFATSLYSMTIKGTS 305
Db 244 SIPAYIAETLYAMKAGCTDHTLIRVMSRSEIDLFNIRKFRKPFATSLYSMTIKGTS 303
QY 306 GDYKALLLLC-GEED 320
Db 304 GDYKALLLLC-GEED 319

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RESULT 4

ANX5 RAT

ID ANX5 RAT STANDARD; PRT; 318 AA.

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AC P14668;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)

```

DE (CBP-1) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchoring CII).
GN ANXAS OR ANX5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88273202; PubMed=2968983;
RA Pepinsky R.B., Tizard R., Nattaliano R.U., Sinclair L.K.,
RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
RA Pratt D., Wachtel L., Hession C., Frey A.Z., Wallner B.P.;
RT "Five distinct calcium and phospholipid binding proteins share
RT homology with lipocortin I.";
RL J. Biol. Chem. 263:10799-10811(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar;
RX MEDLINE=96035863; PubMed=7556178;
RA Imai Y., Kohsaka S.;
RT "Structure of rat annexin V gene and molecular diversity of its
RT transcripts.";
RL Eur. J. Biochem. 232:327-334(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=93369587; PubMed=8362244;
RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
RT "Rat annexin V crystal structure: Ca(2+)-induced conformational
RT changes.";
RL Science 261:1321-1324(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX TISSUE=Kidney;
RX MEDLINE=96069783; PubMed=7583670;
RA Swartz M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
RT "Ca(2+)-bridging mechanism and phospholipid head group recognition in
RT the membrane-binding protein annexin V.";
RL Nat. Struct. Biol. 2:968-974(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
RX MEDLINE=98272673; PubMed=9609693;
RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swartz M.A., Balch C.,
RA Head J.F., Reizinger G., Dedman J.R., Seaton B.A.;
RT "Mutational and crystallographic analyses of interfacial residues in
RT annexin V suggest direct interactions with phospholipid membrane
RT components.";
RL Biochemistry 37:8004-8010(1998).
RN [6]
RP INTERACTION WITH DNMT1.
RX STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=96301899; PubMed=8667030;
RA Ohsawa K., Imai Y., Ito D., Kohsaka S.;
RT "Molecular cloning and characterization of annexin V-binding proteins
RT with highly hydrophilic peptide structure.";
RL J. Neurochem. 67:89-97(1996).
RN [7]
RP FUNCTION: This protein is an anticoagulant protein that acts as an
RP indirect inhibitor of the thromboplastin-specific complex, which
RP is involved in the blood coagulation cascade.
RN [8]
RP SUBUNIT: Monomer. Binds ATRX and DNMT1.
RN [9]
RP DOMAIN: A pair of annexin repeats may form one binding site for
RP calcium and phospholipid.
RN [10]
RP SIMILARITY: Belongs to the annexin family.
RN [11]
RP SIMILARITY: Contains 4 annexin repeats.
RN [12]
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RP or send an email to: license@isb-sib.ch).

CC EMBL: M21730; AAA4512.1; -
DR EMBL: D42137; BAA07708.1; -
DR EMBL: D42129; BAA07708.1; JOINED
DR EMBL: D42130; BAA07708.1; JOINED
DR EMBL: D63337; BAA07708.1; JOINED
DR EMBL: D42131; BAA07708.1; JOINED
DR EMBL: D42132; BAA07708.1; JOINED
DR EMBL: D42133; BAA07708.1; JOINED
DR EMBL: D42134; BAA07708.1; JOINED
DR EMBL: D42135; BAA07708.1; JOINED
DR EMBL: D42136; BAA07708.1; JOINED
DR PIR: C9250; LURTS.
DR PDB: 2XAN; 30-NOV-94.
DR PDB: 1A8A; 17-JUN-98.
DR PDB: 1A8B; 17-JUN-98.
DR PDB: 1BC0; 13-JAN-99.
DR PDB: 1BC1; 13-JAN-99.
DR PDB: 1BC3; 13-JAN-99.
DR PDB: 1BCW; 13-JAN-99.
DR PDB: 1BCY; 13-JAN-99.
DR PDB: 1BCZ; 13-JAN-99.
DR PDB: 1GSN; 13-MAR-02.
DR PDB: 1N41; 04-FEB-03.
DR PDB: 1N42; 04-FEB-03.
DR PDB: 1N44; 04-FEB-03.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
DR Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
KW Placenta; Acetylation; 3D-structure.
FT INIT MET 0 0
FT REPEAT 20 80 ANNEXIN 1.
FT REPEAT 92 152 ANNEXIN 2.
FT REPEAT 176 236 ANNEXIN 3.
FT REPEAT 251 311 ANNEXIN 4.
FT MOD RES 1 1 ACETYLATION.
FT TURN 10 11
FT HELIX 14 25
FT HELIX 32 39
FT TURN 40 41
FT HELIX 44 58
FT HELIX 62 69
FT HELIX 72 82
FT HELIX 85 97
FT HELIX 104 113
FT HELIX 116 130
FT HELIX 134 141
FT HELIX 144 154
FT HELIX 155 156
FT TURN 155 179
FT HELIX 166 179
FT TURN 180 182
FT HELIX 188 197
FT HELIX 200 214
FT HELIX 218 225
FT HELIX 228 242
FT HELIX 244 256
FT TURN 263 273
FT HELIX 274 277
FT HELIX 278 289
FT HELIX 293 300
FT HELIX 303 313
SQ SEQUENCE 318 AA; 35613 MW; 1A755A7C11FALLICE CRC64;
Query Match 91.5%; Score 1464.5; DB 1; Length 318;
Best Local Similarity 92.1%; Pred. No. 46-68;
Matches 292; Conservative 12; Mismatches 12; Indels 1; Gap

5 LRGTVDTPGPDRAETLRKMKIGTDEBSITLITLRSNAROEISAAPFTLNG
|||||

Db 2 LRGTVDPSGDFGRADAEVLKRAMKGLTDEDSIIILTAASNAQRQIAE3FKTLFGRD 61
 Qy 65 LLDLKSRLTGKPEELIYALMKPSRLYAYELKHALKGAGNEKYLTTITIA3RTPPEELRA 124
 Db 62 LVNDKSKSLTGKPEELIYALMKPSRLYAYELKHALKGAGDEKVLTEIIA3RTPPEELRA 121
 Qy 125 IKQAYEEYSGSLLEDVVDGTSYQYQRMVVLQANRPDPDGIPEAQVEODAOALFQAGE 184
 Db 122 IKQAYEEYSGSLLEDVVDGTSYQYQRMVVLQANRPDPDGIPEAQVEODAOALFQAGE 181
 Qy 185 LKMGDEBEKFTITIGTSVSHLRKVFQKMTISGFQIBETIDRETSQNLQOALLAVKSI 244
 Db 182 LKMGDEBEKFTITIGTSVSHLRKVFQKMTISGFQIBETIDRETSQNLQOALLAVKSI 241
 Qy 245 RSIPIAYLAETLYAMKAGAGTDHDLIRVAVRSSEIDLFNIRKFRKQFATSLYSMIKQDT 304
 Db 242 RSIPIAYLAETLYAMKAGAGTDHDLIRVAVRSSEIDLFNIRKFRKQFATSLYSMIKQDT 301
 Qy 305 SGDYKKAALLILC-GEED 320
 Db 302 SGDYKKAALLILC-GEED 318

RESULT 5

ANX5_CHICK STANDARD, PRT, 321 AA.
 AC P17153,
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-1) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplasmin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchotin CIT).
 DE ANX5 OR ANX5.
 GN Gallus gallus (chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.
 OX NCBI_TaxID=9031,
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=8166917; PubMed=2833522;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K.,
 RT "The structure of anchotin CIT, a collagen binding protein isolated from chondrocyte membrane."
 RL J. Biol. Chem. 263:5921-5925(1988).
 RN [2]
 RP SUGGEST SEQUENCING ERROR.
 RX MEDLINE=9020458; PubMed=2552626;
 RA Moss S.E., Crumpton M.J.,
 RT "Alternative splicing or cloning artefact?";
 RL Trends Biochem. Sci. 14:325-325(1989).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=90243721; PubMed=2159478;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K.,
 RT "The structure of anchotin CIT, a collagen binding protein isolated from chondrocyte membrane."
 RL J. Biol. Chem. 265:8344-8344(1990).
 RN [4]
 RP REVISIONS.
 RX Pfaeffle M., Ruggiero F., Hofmann H., Fernandez M.P., Selmin O., Yamada Y., Gairone R., von der Mark K.,
 RL EMBO J. 9:1336-1336(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Liver;
 RX MEDLINE=94215900; PubMed=8163186;
 RA Fernandez M.P., Fernandez M.R., Morgan R.O.,
 RT "Structure of the gene encoding anchotin CIT (chick annexin V).";

RL Gene 141:179-186(1994).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=93249384; PubMed=8484740;
 RA Boustead C.M., Brown R., Walker J.H.,
 RT "Isolation, characterization and localization of annexin V from chicken liver."
 RL Biochem. J. 291:601-608(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93229489; PubMed=8471604;
 RA Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.,
 RT "Structure of chicken annexin V at 2.25-A resolution."
 RL Biochemistry 32:3923-3929(1993).
 CC -1- FUNCTION: Collagen-binding protein.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
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 CC -----
 DR EMBL: M30971; AAA48591.1; ALT_SEQ.
 DR EMBL: U01680; AAB39917.1; JOINED.
 DR EMBL: U01671; AAB39917.1; JOINED.
 DR EMBL: U01672; AAB39917.1; JOINED.
 DR EMBL: U01673; AAB39917.1; JOINED.
 DR EMBL: U01675; AAB39917.1; JOINED.
 DR EMBL: U01676; AAB39917.1; JOINED.
 DR EMBL: U01677; AAB39917.1; JOINED.
 DR EMBL: U01678; AAB39917.1; JOINED.
 DR EMBL: U01679; AAB39917.1; JOINED.
 DR PIR: A35381; LUCH5.
 DR PDB: 1ALA; 31-OCT-93.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 FT REPEAT 24
 FT REPEAT 96 156 ANNEXIN 1.
 FT REPEAT 180 240 ANNEXIN 2.
 FT REPEAT 255 315 ANNEXIN 3.
 FT CONFLICT 168 168 ANNEXIN 4.
 FT TURN 13 14 D -> E (IN REF. 1).
 FT TURN 17 18
 FT HELIX 17 28
 FT HELIX 35 44
 FT HELIX 47 61
 FT HELIX 65 72
 FT HELIX 75 85
 FT TURN 88 90
 FT HELIX 91 100
 FT HELIX 107 116
 FT HELIX 119 133
 FT HELIX 137 144
 FT HELIX 147 157
 FT TURN 158 158
 FT HELIX 159 184
 FT TURN 185 187
 FT HELIX 191 200
 FT HELIX 203 217
 FT HELIX 221 224
 FT HELIX 232 245
 FT HELIX 247 259

FT HELIX 266 275
 FT TURN 276 280
 FT HELIX 281 292
 FT HELIX 296 303
 FT HELIX 306 316
 SQ SEQUENCE 321 AA; 36198 MW; 43E2983F86797025 CRC64;

Query Match 80.6%; Score 1289; DB 1; Length 321;
 Best Local Similarity 78.4%; Pred. No. 1.1e-76;
 Matches 251; Conservative 38; Mismatches 31; Indels 0; Gaps 0;

QY 1 MAQVLRGVTDFPGEDERADAETLRKAMKGLGTDEESITLTLSRSNAQROEISAARKTL 60
 DB 1 MAKYRGVTAFSPFADADAETLRKAMKMGDEETITKILTSRNNAQROEIASAKTL 60
 QY 61 FGRLDLDLKSSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPE 120
 DB 61 FGRLDLDLKSSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPE 120
 QY 121 ELRAIKQVVEEYSGSLDDVVDGTSGYQRMVVLQANRPDAGIDEAQVEDQAQALF 180
 DB 121 EVQNIKQVYMOEYEAULEDKITGETSGHFORLVLQANRPDGRVDEALYKDAQVLF 180
 QY 181 QAGELKMGDEEKEFTITFGTSVSHLRKVPDKYMTISGFQIETITDETSGNLEQULLAV 240
 DB 181 RAGELKMGDEEFTITLTGTSVSHLRKVPDKYMTISGFQIETITDETSGNLEKULLAV 240
 QY 241 VKSIRSIPAVLAETLYYAMKAGTDHDTLIRVMSRSEIDLFNIRKEFRNFPATSLYSMT 300
 DB 241 VKCIRSVPAVFATLYYSMKAGTDHDTLIRVMSRSEIDLIRHEFRNFPATSLYOMI 300
 QY 301 KGDTSGDYKALLLGCEDD 320
 DB 301 QKDTSGDYKALLLGCEDD 320

RESULT 6

ANX5_CYNPY STANDARD; PRT; 323 AA.

ID ANX5_CYNPY STANDARD; PRT; 323 AA.
 AC P70075;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
 NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Yamamoto T., Hikono T., Abe S.I.;
 RT "Differential expression of annexin V during spermatogenesis in the
 RT newt Cynops pyrrhogaster.";
 RL Dev. Genes Evol. 206:64-71 (1996).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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CC EMBL, D64134; BAA11012.1; -
 DR HSSP; P08758; IAVH.
 DR InterPro; IPR001464; Annexin.

DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR Prodom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR KX Annexin; Calcium/phospholipid-binding; Repeat.
 FT REPEAT 26 86 ANNEXIN 1.
 FT REPEAT 98 158 ANNEXIN 2.
 FT REPEAT 182 242 ANNEXIN 3.
 FT REPEAT 257 317 ANNEXIN 4.
 SQ SEQUENCE 323 AA; 35981 MW; 04AB31AC28164CE2 CRC64;

Query Match 68.5%; Score 1096; DB 1; Length 323;
 Best Local Similarity 68.3%; Pred. No. 3.4e-64;
 Matches 215; Conservative 45; Mismatches 55; Indels 0; Gaps 0;

QY 6 RGTVDPPGDERADAETLRKAMKGLGTDEESITLTLSRSNAQROEISAARKTLFGR 60
 DB 8 KGTVDAPDPNDKEDAEITLRKAMKGLGTDEETITKILTSRSNAQROEISARKTLFGR 60
 QY 66 LDDLSKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPE 120
 DB 68 TDDLSKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPE 120
 QY 126 KQYEEYSGSLDDVVDGTSGYQRMVVLQANRPDAGIDEAQVEDQAQALF 180
 DB 128 KETYSKPEPSDLEKIVGDTSGNFERLVLQANRPDGVKDEGVENDAKALF 180
 QY 186 KMGTDSEKFTITFGTSVSHLRKVPDKYMTISGFQIETITDETSGNLEQULLAV 240
 DB 188 KMGTDSEFTISLTGTSVSHLRKVPDKYMTISGFQIETITDETSGNLEKULLAV 240
 QY 246 SIPAVLAETLYYAMKAGTDHDTLIRVMSRSEIDLFNIRKEFRNFPATSLYSMT 300
 DB 248 SIQYLAEVYYSMKAGTDHDTLIRVMSRSEIDLIRHEFRNFPATSLYOMI 300
 QY 306 GDYKALLLGCEDD 320
 DB 308 GDYRANLILGCEDD 322

RESULT 7

ANX6_MOUSE STANDARD; PRT; 672 AA.

ID ANX6_MOUSE STANDARD; PRT; 672 AA.
 AC P14824;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANXA6 OR ANX6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA MELIUB=89030687; PubMed=2972541;
 RT "Molecular cloning of murine p68, a Ca2+-binding protein of the
 RT lipocortin family.";
 RL Eur. J. Biochem. 177:21-27 (1988).
 CC -1- FUNCTION: May associate with CD21. May regulate the release of
 CC Ca2+ from intracellular stores.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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CC EMBL; X13460; CAA31808.1; -
 CC PIR; S01786; S01786.
 DR HSSP; P79134; IAVC.
 DR MGI; 88255; Annex6.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 8.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 8.
 DR SMART; SM00335; ANX; 8.
 DR PROSITE; PS00223; ANNEXIN; 8.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 KW INIT MET 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 SQ SEQUENCE 672 AA; 75755 MW; 2D85C1DD235FC76 CRC64;

Query Match 58.9%; Score 942; DB 1; Length 672;
 Best Local Similarity 59.4%; Pred. No. 7.7e-54;
 Matches 187; Conservative 49; Mismatches 79; Indels 0; Gaps 0;

QY 6 RGVTVDPGPFDERADAEETLRKAMKGLTDESEITLTLSNNOBOEISAAFTLIGRDL 65
 DB 10 RGVVHPPEPDANOQDAALYAMKGRSDKESITLITSSNNOKROICQSYSLGKDL 69
 QY 66 LDDKSELGTGFEKELIVAMKPSRLYDAVELKHALKGATNEKYLTEIISRTPEELRAI 125
 DB 70 IEDLTKELTGKFERLLVNMRLPLAYODAKIKDAISIGIGDEKCLIEILASKNEQHQDL 129
 QY 126 KOYEEYSSLEDDVVDGTSYGYQMLVLLQANDPDAGIDAEQVEDDAALFOAGEL 185
 DB 130 VAAVKDAVERDELSIDTIGDSHFQKMLVLLQGTRENDVVEDLVQDDVYDLVEAGEL 189
 QY 186 KMGTDSEKITTIGTSSVSHLRVPEPKMTISFOLEITDRTSGNLEQOLIAVVKISIR 245
 DB 190 KMGTDGAQPIYILIGNSKOHLRLVPEYIKTKTEKPIEASIRGELSGDFEKLMLAVVKIR 249
 QY 246 SIPAVLAETLYYAMKAGTDDHDLIVMVSRSRIDLFNIRKERRKMFATSLVSMIKGDS 305
 DB 250 STPEYFAERLFRAMKGLGRDNTLIRIVWSRSELDMLDIRIETRYEKSLVSMIKNDS 309
 QY 306 GDYKALLLLCGDD 320
 DB 310 GEYKALMLLCGGDD 324

RESULT 8
 ANX4 HUMAN STANDARD; PRT; 318 AA.
 ID ANX4_HUMAN
 AC P09525; Q96F33; Q9BWK1;
 DT 01-MAR-1989 (Rel. 10; Created)
 DT 01-OCT-1996 (Rel. 34; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Annexin A4 (Annexin IV) (lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAF-II) (PpA-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/41).
 DE (P33/41).
 GN ANX4 OR ANX4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88309022; PubMed=2970257;
 RA Grundmann U., Amann E., Abel K.-J., Kuepper H.A.;
 RT "Isolation and expression of cDNA coding for a new member of the phospholipase A2 inhibitor family.";
 RL Behring Inst. Mitt. 82:59-67(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92155721; PubMed=134676;
 RA Tait J.F., Smith C., Frankberry D.A., Miao C.H., Adler D.A.,
 RA Distchech C.M.;
 RT "Chromosomal mapping of the human annexin IV (ANX4) gene.";
 RL Genomics 12:313-318(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9729215; PubMed=9084877;
 RA Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
 RA Matsumoto I.;
 RT "Characterization of human p33/41 (annexin IV), a Ca2+ dependent carbohydrate-binding protein with monoclonal anti-annexin IV antibodies, AS11 and AS17.";
 RL Biol. Pharm. Bull. 20:224-229(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Eye, and Uterus;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 26-55; 98-123 AND 279-307.
 RX MEDLINE=8906652; PubMed=2974032;
 RA Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
 RA de Haen C.;
 RT "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor.";
 RL J. Biol. Chem. 263:18657-18663(1988).
 RN [6]
 RP SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
 RX MEDLINE=89118212; PubMed=2975506;
 RA Tate J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
 RA Hendrickson L.E., Fujikawa K.;
 RT "Placental anticoagulant proteins: isolation and comparative characterization four members of the lipocortin family.";
 RL Biochemistry 27:6268-6276(1988).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=91073383; PubMed=2254922;
 RA Fremont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;
 RT "Crystallization and preliminary x-ray crystallographic studies of human placental annexin IV.";
 RL J. Mol. Biol. 216:219-221(1990).
 CC -I- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).

RESULT 9	
ANX4_PIG	
ID _ANX4_PIG	STANDARD;
AC P08132; Q29306;	PRT; 318 AA

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QY      7 GTVNDPEPDEBDAETLRKAMKGIGTDEBSILTLRSNAOKOISAAEFLGR  
       |||   ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db      5 GTVKASGFENAAEDQTLRKAMKGIGTDEDLISVLAYRSTPRQEIINTAYKSTIGR
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QY 67 .DDLKSELTKFEKLI VALMKPSRLYDAYELKHALKAGAGTNEKVLTEIIASRTPEELRAIK 126
D 65 DDLKSELTKFEKLI VALMKPSRLYDAYELKHALKAGAGTNEKVLTEIIASRTPEELRAIK 124
QY 127 QVYEEEGSSLEDDVVGDTSGYQRMVYLQANRDPDAGIDEAQVEDQALFQAGELK 186
D 125 QVYEEEGSSLEDDVVGDTSGYQRMVYLQANRDPDAGIDEAQVEDQALFQAGELK 184
QY 187 WGTDEEFITFGRSVSHLRKVPDKYMTISGFOIEITIDETSNGNEQLLAVYKSIKS 246
D 185 WGTDEEFITFGRSVSHLRKVPDKYMTISGFOIEITIDETSNGNEQLLAVYKSIKS 244
QY 247 IPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMTKQDTS 306
D 245 KSAFAERLYKSMKGLGTDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMTKQDTS 304
QY 307 DYKXALLLCGEDD 320
D 305 DYKXALLLCGEDD 318
RESULT 10
ANX6_RAT
ID ANX6_RAT STANDARD; PRT; 672 AA.
AC P48037;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CP3-II)
DE (Calcium-binding protein CATA 65/67).
GN ANX6 OR ANX6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; Tissue=liver;
RA MEDLINE=9531313; PubMed=7607247;
RA Fan H., Josic D., Lim Y.P., Reutter W.;
RT "cDNA cloning and tissue-specific regulation of expression of rat
RT calcium-binding protein 65/67. Identification as a homologue of
RT annexin VI."
RT Eur. J. Biochem. 230:741-751 (1995).
CC - FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores.
CC - DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC - MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC - SIMILARITY: Belongs to the annexin family.
CC - SIMILARITY: Contains 8 annexin repeats.
CC -----
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CC -----
DR EMBL; X86086; CAA60040.1; -
DR PIR; S65683; S52844.
DR HSSP; P79134; IAVC.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 7.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INIT_MET 0 0
FT BY SIMILARITY.

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FT REPEAT 28 88 ANNEXIN 1.
FT REPEAT 100 160 ANNEXIN 2.
FT REPEAT 184 244 ANNEXIN 3.
FT REPEAT 259 319 ANNEXIN 4.
FT REPEAT 371 431 ANNEXIN 5.
FT REPEAT 443 503 ANNEXIN 6.
FT REPEAT 532 592 ANNEXIN 7.
FT REPEAT 607 667 ANNEXIN 8.
SQ SEQUENCE 672 AA; 75622 MW; BBET798A9CAB1511 CRC64;
Query Match 58.2%; Score 931; DB 1; Length 672;
Best Local Similarity 59.0%; Pred. No. 4e-53;
Matches 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;
QY 6 RGVTVTFPGDEBADAETLRKAMKGLGTDDESITLTLSRSNAQROEISAFTLFGRL 65
D 10 RGVTVTFPGDEBADAETLRKAMKGLGTDDESITLTLSRSNAQROEISAFTLFGRL 69
QY 66 LDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKAGAGTNEKVLTEIIASRTPEELRAI 125
D 70 LDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKAGAGTNEKVLTEIIASRTPEELRAI 129
QY 126 KQYEEEGSSLEDDVVGDTSGYQRMVYLQANRDPDAGIDEAQVEDQALFQAGEL 185
D 130 KQYEEEGSSLEDDVVGDTSGYQRMVYLQANRDPDAGIDEAQVEDQALFQAGEL 189
QY 186 KMGTDSEKFTTIGRSVSHLRKVPDKYMTISGFOIEITIDETSNGNEQLLAVYKSIKS 245
D 190 KMGTDSEKFTTIGRSVSHLRKVPDKYMTISGFOIEITIDETSNGNEQLLAVYKSIKS 249
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMTKQDTS 305
D 250 SIPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKFNATSLYSMTKQDTS 309
QY 306 GYKXALLLCGEDD 320
D 310 GYKXALLLCGEDD 324
RESULT 11
ANX6_HUMAN
ID ANX6_HUMAN STANDARD; PRT; 672 AA.
AC P08133;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CP3-II).
GN ANX6 OR ANX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA MEDLINE=88196081; PubMed=3258820;
RA Crumpson M.R., Owens R.J., Tortly N.F., Moss S.E., Waterfield M.D.,
RA Crumpson M.J.;
RT "Primary structure of the human, membrane-associated Ca2+-binding
RT protein p68 a novel member of a protein family."
RT EMBO J. 7:21-27 (1988).
[2]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE=88124902; PubMed=2963335;
RA Suedhof T.C., Slaughter C.A., Leznicki I., Barjon P., Reynolds G.A.;
RT "Human 67-kDa calelectrin contains a duplication of four repeats
RT found in 35-kDa lipocortins."
RL Proc. Natl. Acad. Sci. U.S.A. 85:664-668 (1988).
[3]
SEQUENCE FROM N.A.
RA MEDLINE=89380132; PubMed=2528541;
RA Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya T.,
RA Saino Y., Shidara Y., Maki M.;

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RT "Structure and expression of cDNA for calphobindin II, a human
RT placental coagulation inhibitor."
RL J. Biochem. 106:43-49 (1989).
RN [4]
RX MEDLINE=90236978; PubMed=2139657;
RA Yoshizaki H., Mizoguchi T., Arai K., Shiratsuchi M., Shidara Y.,
RT Makl M.;
RT "Structure and properties of calphobindin II, an anticoagulant
RT protein from human placenta."
RL J. Biochem. 107:43-50 (1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS):
RX MEDLINE=96326697; PubMed=8709144;
RA Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann S.,
RA Huber R., Voges D.;
RT "The structure of recombinant human annexin VI in crystals and
RT membrane-bound";
RL J. Mol. Biol. 260:638-643 (1996).
CC -1- FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores.
CC -1- INDUCTION: By EBV.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- PTM: Phosphorylated in response to growth factor stimulation.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 8 annexin repeats.
CC -----
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CC -----
DR EMBL: D00510; BAA00400.1; -;
DR EMBL: Y00097; CA68286.1; -;
DR EMBL: J03578; AAA35636.1; -;
DR EMBL: BC017046; AAH17046.1; -;
DR PIR: J00032; ACHU68.
DR PDB: 1M91; 15-APR-03.
DR GeneW: HGNC:544; ANXA6.
DR MIM: 114070; -;
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 8.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 8.

DR SMART: SM00335; ANX; 8.
DR PROSITE: PS00223; ANNEXIN; 8.
KW Annexin; Calcium/phospholipid-binding; Repeat; Acetylation;
KW phosphorylation; 3D-structure.
FT INIT_MET 0 0
FT REPEAT 28 88 ANNEXIN 1.
FT REPEAT 100 160 ANNEXIN 2.
FT REPEAT 184 244 ANNEXIN 3.
FT REPEAT 259 319 ANNEXIN 4.
FT REPEAT 371 431 ANNEXIN 5.
FT REPEAT 443 503 ANNEXIN 6.
FT REPEAT 532 592 ANNEXIN 7.
FT REPEAT 607 667 ANNEXIN 8.
FT MOD_RES 1 1 ACETYLATION.
FT REPEAT 1 1 IE -> MK (IN REF. 2).
FT CONFLICT 225 226 E -> T (IN REF. 2).
FT CONFLICT 554 554 E -> D (IN REF. 1).
FT CONFLICT 618 618
SQ SEQUENCE 672 AA; 75742 MW; 2829237029BDIDCB CRC64;

Query Match 57.9%; Score 927; DB 1; Length 672;
Best Local Similarity 57.8%; Pred. No. 7.2e-53;
Matches 182; Conservative 52; Mismatches 81; Indels 0; Gaps 0;

QY 6 RCTVDPFGEDERADAEITLRKAMKGLGTEDESIITLTLSRSNAQROETISAFKTLFGRL
DB 10 RSHIDPFGPDNDQAEALYTMKGFSGDKXALIDITISRSRKQROEVQGSYSLYKGI
QY 66 LDDLSKSELTKFEKLTVALMKPSRLYDAVELHALKAGATNKVLTETIASRTPBELRR
DB 70 IADLKVELTKFERLVLGLMRPAICDAKEIDALISGICTDKCLIELASTNEGMH
QY 126 KQVEEYSSSLDDVDVGTSGYQRMVLLQANRPDAGIDEAQVEDQALFQAG
DB 130 VAAVDAVRDLEADIIQTSHPQMLVLLQGTREDDVSEDLVQDDVDLYEAG
QY 186 KWTDEKFTITGTRSVSHLRKVPDKTWTITSGFOIEETIDETSGNLEQLLAVKKS
DB 190 KMGTDQAQFIYILGNRSKQHLRLVFEDEYLTGKPTIASIRELSGDFEKLMLAVKCY
QY 246 SIPAVIAETLYAMGAGCTDDTLIRVWMSRSEIDLFINRKEPRKNFATSLYSMIGDDP
DB 250 STPEYFAERLFRAMGGLGTRDWTLIRIWSRSELDMLDRELFRTEKSLYSMLKND
QY 306 GDYKATLLTGCEDD 320
DB 310 GEYKTKLTKSGDD 324

RESULT 12
ANX4_MOUSE
ID ANX4_MOUSE STANDARD; PRT; 318 AA.
AC P97429;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Annexin A4 (Annexin IV).
GN ANXA4 OR ANXA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RA Sable C.L., Shannon J., Riches D.W.H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
CC membrane fusion and is involved in exocytosis (by similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
CC (by similarity).
CC -1- SIMILARITY: Belongs to the annexin family.

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CC -!- SIMILARITY: Contains 4 annexin repeats.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U72941; AAB40697.1; -.
DR HSSP: P13214; IANN.
DR MGP: MGI:88030; Anxa4.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
DR Annexin; Calcium/phospholipid-binding; Repeat.
DR INIT MET 0 82 ANNEXIN 1.
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
SQ SEQUENCE 318 AA; 35858 MW; 53FAC7AD8006BCD CRC64;

Query Match 57.9%; Score 926; DB 1; Length 318;
Best Local Similarity 57.6%; Pred. No. 3,4e-53;
Matches 181; Conservative 58; Mismatches 75; Indels 0; Gaps 0;

QY 7 GTVDFPFPEDRRADDELTKKMKKGLGDEESILLTTSRSNAQROETSAFETLFGRL 66
Db 5 GTVKAASSFNATETEDQTRKMKKGLGDEDAITGLAVRNPAQREISAVTSTGRDLI 64
QY 67 DDLKSELGKFEKTLVALMKPSRLYDAYELKHALKAGATNKEVTEITATSPERLRAIK 126
Db 65 EDLSELSNNEEQVILGIMTPTVLYDVELRKAMKAGTIDGCLIEILASTPEIRKIN 124
QY 127 QVEEERYSGLLEDDVVGDTSGYQRMVLLQANNDPAGIDEAQVEQDAQFLPQAGELK 186
Db 125 QTYQOQGRSLIEDIDCSPTSPMPQRLVFLSAAGDEBNYLDLMLKQDAQLVEAGSKR 184
QY 187 WGTDEKFTTFGRSRVSHLKKVPDKYWTISGFOEETIDETSQNTLEQLLAVKSTRS 246
Db 185 WGTDEVKFLSLICSRNRHLLHVEDEYKRIQKIDIEQIKSETSGSFEDALLAIKCMS 244
QY 247 IPATLAETLYAMKAGTDDHTLLRWVSRSEIDLFRNKEFRKFAISLYEMIKGDTSG 306
Db 245 KPSYFAERLYKSMKGLGTDNTLLRWVSRRAEIDMLDIRASFRLYGRSLYEFKGDTS 304
QY 307 DYKALALLCGEDD 320
Db 305 DYKRVLLILCGDD 318

RESULT 13
ANXA_BOVIN STANDARD; PRT; 318 AA.
ID ANXA_BOVIN STANDARD; PRT; 318 AA.
AC P13214;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A4 (Annexin IV) (lipocortin IV) (Endomexin I) (Chromobindin 4)
DE (Protein II) (P32.5) (placental anticoagulant protein II) (PAP-II)
DE (P34-X) (35-beta calmodulin) (Carbohydrate-binding protein P33/P41)
DE (P33/41).
DE ANXA4 OR ANXA.
GN ANXA4 OR ANXA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89050088; PubMed=2847715;
RA Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
RT "Cloning and characterization of a cDNA encoding bovine endomexin
RT (chromobindin 4).";
RL Biochem. Biophys. Res. Commun. 156:660-667(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96205957; PubMed=6631806;
RA Kojima K., Yamamoto K., Irimura T., Ogawa T., Ogawa H., Matsumoto I.;
RT "Characterization of carbohydrate-binding protein p33/41: relation
RT with annexin IV, molecular basis of the doublet forms (p33 and p41),
RT and modulation of the carbohydrate binding activity by
RT phospholipids.";
RL J. Biol. Chem. 271:7679-7685(1996).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sutton R.B., Sprang S.R.;
RL Submitted (SEP-1995) to the PDB data bank.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=98070213; PubMed=9405281;
RA Zanotti G., Malpeli G., Glubich F., Follì C., Scopinì M., Olivè L.,
RA Savio A., Berni R.;
RT "Structure of the trigenal crystal form of bovine annexin IV.";
RL Biochem. J. 329:101-106(1998).
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M22248; AAA30507.1; -.
DR EMBL: X13627; CAA31954.1; -.
DR EMBL: D78178; BAA11243.1; -.
DR PIR: A31578; LUBO4.
DR PDB: IANN; 29-JAN-96.
DR PDB: IAOV; 14-JAN-98.
DR PDB: 114A; 25-APR-01.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
FT INIT MET 0
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
FT CONFLICT 94 94 L -> V (IN REF. 2).
FT CONFLICT 210 210 E -> K (IN REF. 2).
FT HELIX 15 26
FT HELIX 33 40
FT TURN 41 42
FT HELIX 45 59
FT HELIX 63 70
FT HELIX 73 83
FT HELIX 86 98
FT HELIX 105 114
FT HELIX 117 131

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FT HELIX 135 142
 FT HELIX 145 155
 FT TURN 156 156
 FT HELIX 167 182
 FT TURN 183 185
 FT HELIX 189 198
 FT HELIX 201 215
 FT HELIX 219 226
 FT HELIX 229 257
 FT HELIX 264 274
 FT TURN 275 278
 FT HELIX 279 280
 FT HELIX 294 301
 FT HELIX 304 314
 SQ SEQUENCE 318 AA; 35757 MW; 86BDBDF349D774FD CRC64;

Query Match 57.8%; Score 924; DB 1; Length 318;
 Best Local Similarity 58.3%; Pred. No. 4,6e-53;
 Matches 183; Conservative 51; Mismatches 80; Indels 0; Gaps 0;

QY 7 GTVTDPGDERADAEFTLRKAMKGLTDEESITLTLSRSNAQOEISAFTLFGDRL 66
 DB 5 GTVKASGFGNAEDAGTLRKAMKGLTDEDAIIVLAYSTAQOEIRTAHYTTIGRDL 64
 QY 67 DDLKSELTGKFEKLIYALMKPSRLYDAVELKALKAGATNEKVTETIISRTPEELRAIK 126
 DB 65 DDLKSELGSGFEQVILGMPTITVLVVOELRRAMKAGDEGLIILASRTPEELRIIN 124
 QY 127 QVVEEYSGSLLEDVVDGTSGYQRMVLLQANRPDAGIDEAQVEQDAQALFOAGEIK 186
 DB 125 QTYOLOYGRSLEDISDTSFMQVILVLSAGGRDESNVLDALMKRQDAQDLYEAGEKK 184
 QY 187 WGTDEEKFTITFGTSVSHLRKVPDKYMTISGFQIETITDRETSNLEQLLAVMSIS 246
 DB 185 WGTDEVKFLTLVLCSSRNHLLAHVFDEYKRIAQKIDEGISKESTSGSFEDLLAIVKCMRN 244
 QY 247 IPAYLAETLYAMKAGCTDHTILIRWVSGSEIDLFRKEPKNFATSLYSMIKGTSG 306
 DB 245 KSAVFAERLYKSMKGLCTDDTLIRWVSAEIDMDIRANFRLYGKSLYSFTKGTSG 304
 QY 307 DYKALLLLCGEDD 320
 DB 305 DYRKVLLILCGGD 318

RESULT 14
 ANX4 CANFA STANDARD; PRT; 318 AA.
 ID ANX4 CANFA
 AC P50994;
 DT 01-OCT-1996 (Rel. 34, Last Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A4 (Annexin IV) (lipocortin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).
 GN ANX4 OR ANX4.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N. A. AND SEQUENCE OF 78-95 AND 134-149.
 RC STRAIN=Mongrel; Tissue=Pancreas;
 RX MEDLINE=22015264; PubMed=12020832;
 RA Fukuoaka S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.,
 RT "Cloning and characterization of ZAP36, an annexin-like, zymogen granule membrane associated protein, in exocrine pancreas";
 RL Biochim. Biophys. Acta 1575:148-152(2002).
 RN [2]
 RP SEQUENCE OF 1-9.
 RX MEDLINE=94362286; PubMed=7765250;
 RA Fukuoaka S.-I.;
 RT "Analysis of ZAPs, zymogen granule membrane associated proteins, in the regulated exocytosis of the pancreas";

RL Biosci. Biotechnol. Biochem. 58:1282-1285(1994).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity (By similarity).
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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 CC EMBL; D38223; BAA07398.1; -.
 DR HSP; P13214; IANX.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR Prodom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 FT INIT MET 0 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 138 138 V -> D (IN REF. 1; AA (SEQUENCE)).
 SQ SEQUENCE 318 AA; 35681 MW; 42EF5B89179B4863 CRC64;

Query Match 56.9%; Score 911; DB 1; Length 318;
 Best Local Similarity 57.3%; Pred. No. 3.2e-52;
 Matches 180; Conservative 54; Mismatches 80; Indels 0; Gaps

QY 7 GTVTDPGDERADAEFTLRKAMKGLTDEESITLTLSRSNAQOEISAFTLFGDRL 66
 DB 5 GTVKASGFGNATEDAGTLRKAMKGLTDEDAIIVLAYSTAQOEIRTAHYTTIGRDL 64
 QY 67 DDLKSELTGKFEKLIYALMKPSRLYDAVELKALKAGATNEKVTETIISRTPEELRAIK 126
 DB 65 DDLKSELGSGFEQVILGMPTITVLVVOELRRAMKAGDEGLIILASRTPEELRIIN 124
 QY 127 QVVEEYSGSLLEDVVDGTSGYQRMVLLQANRPDAGIDEAQVEQDAQALFOAGEIK 186
 DB 125 QTYOLOYGRSLEDISDTSFMQVILVLSAGGRDESNVLDALMKRQDAQDLYEAGEKK 184
 QY 187 WGTDEEKFTITFGTSVSHLRKVPDKYMTISGFQIETITDRETSNLEQLLAVMSIS 246
 DB 185 WGTDEVKFLTLVLCSSRNHLLAHVFDEYKRIAQKIDEGISKESTSGSFEDLLAIVKCMRN 244
 QY 247 IPAYLAETLYAMKAGCTDHTILIRWVSGSEIDLFRKEPKNFATSLYSMIKGTSG 306
 DB 245 KSAVFAERLYKSMKGLCTDDTLIRWVSAEIDMDIRANFRLYGKSLYSFTKGTSG 304
 QY 307 DYKALLLLCGEDD 320
 DB 305 DYRKVLLILCGGD 318

RESULT 15
 ANX6 CHICK STANDARD; PRT; 671 AA.
 ID ANX6 CHICK
 AC P51901;
 DT 01-OCT-1996 (Rel. 34, Last Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (p68) (P70) (Protein III) (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).

GN ANXA6 OR ANX6.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94092130; PubMed=8267590;
 RA Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthier R.E.;
 RT "Characterization, cloning and expression of the 67-kDa annexin from
 RT chicken growth plate cartilage matrix vesicles."
 RL Biochem. Biophys. Res. Commun. 197;556-561(1993).
 CC -1- FUNCTION: May associate with CD21. May regulate the release of
 CC Ca(2+) from intracellular stores (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; S67466; AB29337.2; -
 DR PIR; J02029; J02029.
 DR HSSP; P79134; IAVC.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 8.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 8.
 DR SMART; SM00335; ANX; 8.
 DR PROSITE; PS00223; ANNEXIN; 5.
 DR KMW; Annexin; Calcium/phospholipid-binding; Repeat.
 FT REPEAT 27 87 ANNEXIN 1.
 FT REPEAT 99 159 ANNEXIN 2.
 FT REPEAT 183 243 ANNEXIN 3.
 FT REPEAT 258 318 ANNEXIN 4.
 FT REPEAT 370 430 ANNEXIN 5.
 FT REPEAT 442 502 ANNEXIN 6.
 FT REPEAT 531 592 ANNEXIN 7.
 FT REPEAT 607 666 ANNEXIN 8.
 SQ SEQUENCE 671 AA; 75218 MW; D0E02F4311A93D98 CRC64;
 Query Match 56.5%; Score 904.5; DB 1; Length 671;
 Best Local Similarity 58.0%; Pred. No. 2.1e-51;
 Matches 185; Conservative 51; Mismatches 82; Indels 1; Gaps 1;
 QY 3 OVLKGTVDPPGFDERADAETLRKAMKGLGTDEESITLTLSRSNOROEISAFFTLRG 62
 DB 6 KYRVSVPKPPGNAQODADALCNAMKGRSDKDALIDLTSSNORLEICQAVSYQ 65
 QY 63 RDLIDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVTETIIASRTPEEL 122
 DB 66 KDLIDLKSELTKGFEKLIIVSLMRPPAYSAKEIKDALINGIGDEKCLEIILASRNQEI 125
 QY 123 RAIKQYEEYSSLEDVVGDTSGYQRMVVLQANRDPDAGIDEAIVEDAQLFQA 182
 DB 126 HDLVAAVYKAYERDEADVVGDTSGHFKMLVVLQGAEREDVVEDVVEDAKOLLRA 185
 QY 183 GELKMGTDDEKFTIFGRSVSHLRKVPFKMNTISFOIEETIDTRETSGNLQOLLIAVVK 242
 DB 186 GELKMGTDDEKFTIFGRSVSHLRKVPFKMNTISFOIEETIDTRETSGNLQOLLIAVVK 245
 QY 243 SIRSIPAYAEETLYYAMKAGTDHDLTIVWTSRSRSDLEFNIRKERRKFAISYSMTMG 302
 DB 246 CRSTAEYFAERLYYAMKAGLGRDNLTHIMWSRSSEIDMLIREVFRTRYKDSLHNMKE 305
 QY 303 DTSGDYKALLILLC-GEED 320

DB 306 DTSGDYKALLILLCGEED 324
 RESULT 16
 ANX4 RAT STANDARD; PRT; 318 AA.
 AC P55260;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A4 (Annexin IV) (lipocortin IV) (36 kDa zymogen granule
 DE membrane associated protein) (ZAP36).
 GN ANXA4 OR ANX4.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar; TISSUE=Pancreas;
 RX MEDLINE=22015264; PubMed=12020832;
 RA Fukuoka S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.;
 RT "Cloning and characterization of ZAP36, an annexin-like, zymogen
 RT granule membrane associated protein, in exocrine pancreas."
 RL Biochim. Biophys. Acta 1575;148-152(2002).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; D38224; BAA07399.2; -
 DR HSSP; P13214; IANN.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR KMW; Annexin; Calcium/phospholipid-binding; Repeat.
 FT INIT MET 0 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 SQ SEQUENCE 318 AA; 35717 MW; FF630ABEA22ED2E7 CRC64;
 Query Match 56.4%; Score 903; DB 1; Length 318;
 Best Local Similarity 56.7%; Pred. No. 1.1e-51;
 Matches 178; Conservative 54; Mismatches 82; Indels 0; Gaps 0;
 QY 7 GTVTDPPGFDERADAETLRKAMKGLGTDEESITLTLSRSNOROEISAFFTLRGDIL 66
 DB 5 GTVKAASGNATEDAQLKAMKGLGTDEDAIIGVLACRNRAQREITAYASTIGRIDL 64
 QY 67 DDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVTETIIASRTPEEL 126
 DB 65 DDLKSELTKGFEKLIIVGMMTPVLVDYQELRRAMKAGTDEGCLIEIILASRNPEIRRN 124
 QY 127 QVYEEYSSLEDVVGDTSGYQRMVVLQANRDPDAGIDEAIVEDAQLFQA 186

Db 125 QTYOQYGRSLIEDICSDTSPFQRLVSLTAGRDEGNVLDLVRDADLYEAGEKR 184
 QY 187 WGTDEBEKFTTFCGRSVSHLRKVPKMTTISGFOIEETIDETSQNLQALLAVKRS 246
 185 WGTDEBEKFTTILCSNRNHLHPDEVKRIQKDIQSIKETSSTSPFDALLATVCKRN 244
 QY 247 IPAYLAETLYAMKAGCTDDHTLLRWVWSRSEIDLFNIRKPKFATSLYMIKGTSG 306
 245 KPAVFAERLYKSMKGLGTDDSTLLRWVWSRAEIDMDLIPANKRVYKSLSTFKGTSG 304
 QY 307 DYKALLLCGEDD 320
 305 DYKVALLLCGGD 318
 Db

RESULT 17
 ANXB_BOVIN STANDARD; PRT; 503 AA.
 ID ANXB_BOVIN P27214; P27215;
 AC P27214; P27215; (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A11 (Annexin XI) (calyculin-associated annexin 50) (CAP-50).
 GN ANXA11 OR ANX11.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Chondrocytes;
 RX MEDLINE=92184796; PubMed=1372001;
 RA Towle C.A., Treadwell B.V.;
 RT "Identification of a novel mammalian annexin. cDNA cloning, sequence analysis, and ubiquitous expression of the annexin XI gene.";
 RL J. Biol. Chem. 267:5416-5423 (1992).
 RN (2)
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Cartilage;
 RX MEDLINE=92305067; PubMed=1535225;
 RA Towle C.A., Weisbach L., Treadwell B.V.;
 RT "Alternatively spliced annexin XI transcripts encode proteins that differ near the amino-terminus.";
 RL Biochim. Biophys. Acta 1131:223-226 (1992).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P27214-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P27214-2; Sequence=VSP 000289;
 CC -I- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
 CC -I- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -I- SIMILARITY: Belongs to the annexin family.
 CC -I- SIMILARITY: Contains 4 annexin repeats.
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 CC EMBL; M82802; AAA30379.1; -
 DR EMBL; Z11742; CAA77801.1; -
 DR PIR; A43113; IUBO11.
 DR PIR; S23447; S23447.
 DR HSSP; P13214; IAWO.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005654; C:nucleoplasm; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.

DR InterPro; IPR001464; Annexin.
 DR Pfam; PF001391; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR PRODOM; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; Alternative splicing.
 FT REPEAT 207 267 ANNEXIN 1.
 FT REPEAT 279 339 ANNEXIN 2.
 FT REPEAT 363 423 ANNEXIN 3.
 FT REPEAT 438 498 ANNEXIN 4.
 FT VARSPLIC 20 56 GGAWGAGAYPEPTPEIGLDNVAVYAGFNQDYLSGV -
 FT VPESHSAGCGQGLFPAAMDRAVSDGPAAMMLAAVLVRAT
 FT (in isoform 2).
 FT /FTID=VSP 000289.
 FT
 SQ SEQUENCE 503 AA; 54018 MW; 3AF6503CCA6D05A1 CEC64;
 Query Match 54.7%; Score 875; DB 1; Length 503;
 Best Local Similarity 55.2%; Pred. No. 1.2e-49;
 Matches 174; Conservative 58; Mismatches 83; Indels 0; Gaps

QY 6 RGTVDPPGPERADAEITRRKAMKGLGTDESIITLLTSRNSAQRQETISAAFKTLFGED
 189 RGTITDAGFPDLDAEVLRRAMGFGTDEQAIIIDCGSRNKRQOILSFKTAYGKD
 Db 66 LDDLKSELTKFPEKILVALMKPSRLDYAYELKALKAGTNEKUTETIIASRTPELRA
 249 IKDLKSELNPFKEKTIILAMKTPVLFDAYEIKEAIKAGTDEACIETILASRSNHIREE
 QY 126 KQVTEEBYGSLEDDVVDGTGYQRMVLQANRPDAGIDEAQVQDQALFQAGE
 309 NRVTKEFEKTLLEAIRSDTSGHFORLLISLQGRDSTVDMTLVORDVELYAAER
 QY 186 KMGDEBEKFTTFCGRSVSHLRKVPKMTTISGFOIEETIDETSQNLQALLAVKRS
 369 RLGTDESKFNAILCSRSRAHVAVAFNEYQRTGRDIEKCSKSGDLEQGLAVAKCI
 Db 246 SIPAYLAETLYAMKAGCTDDHTLLRWVWSRSEIDLFNIRKPKFATSLYMIKGTSG
 429 NTPAFFAERLYKSMKGLGTDDSTLLRWVWSRAEIDMDLIPANKRVYKSLSTFKGTSG
 QY 306 GDYKALLLCGEDD 320
 469 GDYKVALLLCGGD 303
 Db

RESULT 18
 ANXB_RABBIT STANDARD; PRT; 503 AA.
 ID ANXB_RABBIT P33477;
 AC P33477;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A11 (Annexin XI) (calyculin-associated annexin 50) (CAP-50)
 GN ANXA11 OR ANX11.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN (1)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=92378579; PubMed=1380798;
 RA Tokumitsu H., Mizutani A., Muramatsu M.-A., Yokota T., Arai K.-I., Hidaka H.;
 RT "Molecular cloning of rabbit CAP-50, a calyculin-associated annexin protein.";
 RL Biochem. Biophys. Res. Commun. 186:1227-1235 (1992)
 CC -I- FUNCTION: Binds specifically to calyculin in a calcium-dependent manner.
 CC -I- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -I- SIMILARITY: Belongs to the annexin family.

CC -!- SIMILARITY: Contains 4 annexin repeats.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D10883; BAA01705.1; -
 CC PIR: JH0694; LURB11.
 CC HSSP: P13214; IANV.
 CC GO: GO:0005635; C:nuclear membrane; ISS.
 CC GO: GO:0005654; C:nucleoplasm; ISS.
 CC GO: GO:0005515; F:protein binding; ISS.
 CC InterPro: IPR001464; Annexin.
 CC Pfam: PF00191; annexin; 4.
 CC PRINTS: PR00196; Annexin.
 CC ProDom: PD000143; Annexin; 4.
 CC SMART: SMO0335; ANX; 4.
 CC PROSITE: PS00223; ANNEXIN; 4.
 CC Annexin; Calcium/phospholipid-binding; Repeat.
 CC REPEAT 207 267 ANNEXIN 1.
 CC REPEAT 279 339 ANNEXIN 2.
 CC REPEAT 363 423 ANNEXIN 3.
 CC REPEAT 438 498 ANNEXIN 4.
 CC SEQUENCE 503 AA; 54034 MW; 44C15F290770AC9F CRC64;
 SO
 Query Match 54.6%; Score 873; DB 1; Length 503;
 Best Local Similarity 54.6%; Pred. No. 1.6e-49;
 Matches 172; Conservative 60; Mismatches 83; Indels 0; Gaps 0;
 QY 6 RGVYDFGDEPDAETLRAMKGLGDEESITLTLSRNAQOEISAATKTLFGRL 65
 Db 189 RGTITDASGFDPLRDAEVLKRAMKGFQDEQAIDCCSRNKORQQLLSEKTAAYGDL 248
 QY 66 LDDLSKSEITGFEKILVLMKPSRLVDAVELKALKAGNTEKTEITASRTPELR 125
 Db 249 IKDKSELSGNFEKILVLMKPSRLVDAVELKALKAGNTEKTEITASRTPELR 308
 QY 126 KQVEEESGSSLEDDVVDTSYQRMVLVLLQNRDADIGAEQVEQDCAIFQAGEL 185
 Db 309 NKAKTEKTEKTLERIRSDTSQHFQRLISQGRDSTVDMSLVQDVEETVYAGEN 368
 QY 186 KMGDEEKFITIFGRSVSHLRKVPDKYMTISGFIETIDRETSNGNEQLLVASIR 245
 Db 369 RLGTDESKFNALVLSRSRAHVAVFNEYQRMGTGRDIKSIKREMSGDLQMLAVKCLK 428
 QY 246 SIPAYLAETLYAMKAGTDHTLIRVWRSSEIDLFNIRKPEKFNATSLYSMIKQDTS 305
 Db 429 NTPAFPAERLRNARMGATKQRTLIRVWRSSEIDLDIRAEYKRMCKSLYHISGDT 488
 QY 306 GDYKALLLLCGEDD 320
 Db 489 GDYRKILLKICGGND 503
 RESULT 19
 ANXB HUMAN STANDARD; PRT; 505 AA.
 AC P50995;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CA5-50)
 DE (56 kDa autoantigen).
 GN ANXA11 OR ANX11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Teratocarcinoma;
 RX MEDLINE=94140847; PubMed=7508441;
 RA Misaki Y., Pruin G.J.M., van der Kemp A.W., van Venooij W.J.;
 RT "The 56K autoantigen is identical to human annexin XI.";
 RL J. Biol. Chem. 269:4240-4246(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20469408; PubMed=11013079;
 RA Bances P., Fernandez M.R., Rodriguez-Garcia M.I., Morgan R.O.,
 RA Fernandez M.P.;
 RT "Annexin A11 (ANXA11) gene structure as the progenitor of paralogous
 RL annexins and source of orthologous cDNA isoforms.";
 RN Genomics 69:95-103(2000).
 RP [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=12477932; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdi T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguezes S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe U.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC AND POSSIBLY NUCLEAR.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- DISEASE: Antibodies against ANXA11 are present in sera from
 CC patients with various autoimmune diseases, predominantly in sera
 CC from patients with rheumatoid arthritis, systemic lupus
 CC erythematosus, or Sjogren's syndrome.
 CC -!- SIMILARITY: Belongs to the annexin family.
 CC -!- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC EMBL: L19605; AAA19734.1; -
 CC EMBL: AJ278463; CAB94995.1; -
 CC EMBL: AJ278464; CAB94996.1; -
 CC EMBL: AJ278465; CAB94997.1; -
 CC EMBL: BC007564; AA07564.1; -
 CC PIR: A53152; A53152.
 CC HSSP: P13214; IANV.
 CC Genew: HGNC:535; ANXA11.
 CC MIM: 602572; -
 CC GO: GO:0005737; C:cytoplasm; TAS.
 CC GO: GO:0005635; C:nuclear membrane; NAS.
 CC GO: GO:0005654; C:nucleoplasm; NAS.
 CC GO: GO:0005543; F:phospholipid binding; TAS.
 CC GO: GO:0005515; F:protein binding; IPT.
 CC GO: GO:0006955; P:immune response; TAS.
 CC InterPro: IPR001464; Annexin.
 CC Pfam: PF00191; annexin; 4.

PRINTS; PRO196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat; Polymorphism.
FT REPEAT 209 269 ANNEXIN 1.
FT REPEAT 281 341 ANNEXIN 2.
FT REPEAT 365 425 ANNEXIN 3.
FT REPEAT 440 500 ANNEXIN 4.
FT REPEAT 230 230 R -> C (in dbSNP:1049550).
FT VARIANT 457 457 /FTID=VAR_012006.
FT I -> V (in dbSNP:1802932).
FT /FTID=VAR_012007.
SQ SEQUENCE 505 AA; 54389 MW; 4ADCA0CF270BEE4 CRC64;
Query Match 54.1%; Score 865; DB 1; Length 505;
Best Local Similarity 53.7%; Pred. No. 5.3e-49;
Matches 169; Conservative 61; Mismatches 85; Indels 0; Gaps 0;
QY 6 RGTVDTPGDFERADAETLRKAMKGGTDEESILTLITLTSRNASNORQISAAFTLFGRL 65
DB 191 RGTITDAPGDFDLRDAEVLRLKAMKGGTDEQALIDCLGSRSNKQROQILSFTKAYGKL 250
QY 66 LDDLKSELTGKFEKLIYALMKPSRLDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
DB 251 IKDLKSELGSENFKEKTLALMKTPVLFDIYEIKALIGVGTDEACLEIILASNSNEHIREL 310
QY 126 KOVVEEYSSLEDVVGDTSGYGYQMLVVLQANRDPDAGIDEAQVEDQAALFOAGEL 185
DB 311 NRAYKAEFKKTLEAARSDTSIGFQRLISLSQGNRDESNVMSLAQRODAQELVAAEN 370
QY 186 KWTDEKEFTITFGTRSVSHLRKVFDPKXMTISGFQIEETIDRTSGNLEQLLAVYKSR 245
DB 371 RLGTDSEKFNALVCSRAHLVAVFNEYQMTGRDIEKISCREMSGDLLEGMLAVVKKL 430
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMSRSSELDENIKERKKNFATISYMTIGDP 305
DB 431 NTPAFPAERLNKMRGAGTDRILIRIMVSRSELDLDIRSEYKRMVGSYLHDISGDS 490
QY 306 GDYKALLLCGEDD 320
DB 491 GDYKILLKICGND 505
RESULT 20
ANXB MOUSE STANDARD; PRT; 503 AA.
ID ANXB MOUSE P97384;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP-50).
GN ANXA11 OR ANXA11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97092887; PubMed=8938449;
RA Fernandez M.P., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RT "Sequence and chromosomal localization of mouse annexin XI";
RL Genomics 37:366-374(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=20469408; PubMed=11013079;
RA Bances P., Fernandez M.R., Rodriguez-Garcia M.I., Morgan R.O.,
RT "Annexin A11 (ANXA11) gene structure as the progenitor of paralogous
RT annexins and source of orthologous cDNA isoforms";
RL Genomics 69:95-103(2000).

CC - FUNCTION: Binds specifically to calcyclin in a calcium-dependent
CC manner.
CC - DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC - SIMILARITY: Belongs to the annexin family.
CC - SIMILARITY: Contains 4 annexin repeats.
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CC
DR EMBL; U65986; AAB42012.1; -
DR EMBL; AJ289760; CAB94770.1; -
DR EMBL; AJ289761; CAB94770.1; JOINED.
DR EMBL; AJ289762; CAB94770.1; JOINED.
DR EMBL; AJ289763; CAB94770.1; JOINED.
DR EMBL; AJ289764; CAB94770.1; JOINED.
DR EMBL; AJ289765; CAB94770.1; JOINED.
DR EMBL; AJ289766; CAB94770.1; JOINED.
DR EMBL; AJ289767; CAB94770.1; JOINED.
DR EMBL; AJ289768; CAB94770.1; JOINED.
DR EMBL; AJ289769; CAB94770.1; JOINED.
DR HSSP; P13214; IANN.
DR SWISS-2DPAGE; P97384; MOUSE.
DR MGI; MGI:108481; Anxa11.
DR GO; GO:0005635; C:nuclear membrane; ISS.
DR GO; GO:0005654; C:nucleoplasm; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT REPEAT 207 267 ANNEXIN 1.
FT REPEAT 279 339 ANNEXIN 2.
FT REPEAT 363 423 ANNEXIN 3.
FT REPEAT 438 498 ANNEXIN 4.
SQ SEQUENCE 503 AA; 54111 MW; 424B1345E0F4EC8A CRC64;
Query Match 53.6%; Score 857; DB 1; Length 503;
Best Local Similarity 54.0%; Pred. No. 1.7e-48;
Matches 170; Conservative 59; Mismatches 86; Indels 0; Gap


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RESULT 21
ANX8 MOUSE STANDARD; PRT; 327 AA.
ID ANX8_MOUSE 035610;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Annexin A8 (Annexin VIII).
GN ANX8 OR ANX8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Fetal;
RX MEDLINE=9805678; PubMed=9434938;
RA Fernandez M.P., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Morgan R.O.;
RT "The genetic origin of mouse annexin VIII.";
RL Mamm. Genome 9:8-14(1998).
CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplastin-specific complex, which
CC is involved in the blood coagulation cascade (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC -----
DR EMBL: AJ002390; CAA05364.1;
DR HSP: P14668; 1A8B.
DR MGD: MGI:1201374; Anx8.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin.4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin.4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation.
FT REPEAT 38
FT REPEAT 90 ANNEXIN 1.
FT REPEAT 110 162 ANNEXIN 2.
FT REPEAT 195 247 ANNEXIN 3.
FT REPEAT 270 322 ANNEXIN 4.
SQ SEQUENCE 327 AA; 36843 MW; 2CC6163642D29EA0 CRC64;

Query Match 52.7%; Score 842.5; DB 1; Length 327;
Best Local Similarity 57.2%; Pred. No. 9e-48;
Matches 179; Conservative 49; Mismatches 84; Indels 1; Gaps 1;
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QY 247 IPAYLAFTIYVAMKAGCTDHTLIRVAVSRSEIDLFINRKEFRKNPATSLYMTKGTSG 306
DB 254 VHSYFAERLLYAMKAGCTRGDTLRNVSRSSEIDLNIKQFRRKYGKTLSSMTADTSG 313
QY 307 DYKALLLCGED 319
DB 314 YKTKALLNLVGTG 326

RESULT 22
ANX8 HUMAN STANDARD; PRT; 327 AA.
ID ANX8_HUMAN
AC P13928; Q9BTJ4;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A8 (Annexin VIII) (Vascular anticoagulant-beta) (VAC-beta).
GN ANX8 OR ANX8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90032687; PubMed=2530088;
RA Hauptmann R., Maurer-Pogoy I., Krystek E., Bodo G., Andree H.,
RA Reutelingersperger C.P.M.;
RT "Vascular anticoagulant beta: a novel human Ca2+/phospholipid binding
RT protein that inhibits coagulation and phospholipase A2 activity. Its
RT molecular cloning, expression and comparison with VAC-alpha.";
RL Eur. J. Biochem. 185:63-71(1989).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92216091; PubMed=1313714;
RA Chang K.S., Wang G., Freireich E.J., Daly M., Maylor S.L.,
RA Trujillo J.M., Stas S.A.;
RT "Specific expression of the annexin VIII gene in acute promyelocytic
RT leukemia.";
RL Blood 79:1802-1810(1992).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancicreas;
RX MEDLINE=23388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shemen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplastin-specific complex, which
CC is involved in the blood coagulation cascade.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----
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DR EMBL; M16662; CA34650.1; -
DR EMBL; M81844; AAB46383.1; -
DR EMBL; BC004376; AAB4376.1; -
DR EMBL; A07358; CAA00657.1; -
DR PIR; S06476; LUH08.
DR HSSP; P14668; IBCZ.
DR Genew; HGNC:546; ANXA8.
DR MIM; 602396; -
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
KW Placenta; Polymorphism.
FT REPEAT 30 ANNEXIN 1.
FT REPEAT 102 ANNEXIN 2.
FT REPEAT 187 ANNEXIN 3.
FT REPEAT 262 ANNEXIN 4.
FT REPEAT 322 ANNEXIN 4.
FT VARIANT 6 A -> S.
FT /FTID=VAR 000604.
FT Q -> T (IN REF. 2).
FT F -> L (IN REF. 2).
FT R -> S (IN REF. 2).
FT A -> G (IN REF. 2 AND 3).
FT GD -> RV (IN REF. 2).
FT 313 314
SQ SEQUENCE 327 AA; 36879 MW; 3AAEID7072A9379 CRC64;

Query Match 52.0%; Score 832.5; DB 1; Length 327;
Best Local Similarity 56.5%; Pred. No. 4e-47;
Matches 177; Conservative 48; Mismatches 87; Indels 1; Gaps 1;

QY 8 TVTDFPGFDRRAAETLRKAMKGLGTDSEILTLTSSRNAQROEISAARETLFGRIILD 67
DB 14 TVKSSSHFNDDPAETLYKMKKGIGTNEQAIIIVLTRSNTQROQIAKSFQAQFGKDLTE 73
QY 68 DLNSELTKREKTLVAMKCSRLYDAYELKHALKGAGTNEKVLTEIIASRPEELRAIKQ 127
DB 74 TLKSELGKFEERLIVAMYPYRYEAKELHDMKGLTKEGVIIETILASRTKQDLREIMK 133
QY 128 VYEEYSSSLDDVVGDTSGYVQMLVLLQANDP-DAGIDEAQVEQDAQALPQAGELK 186
DB 134 AYEDYSSSLDEEDQADTSGYLERILVCLLGSRDDVVSFVDPALADQADOLYAAAGEKI 193
QY 187 WGTDEEKPTITFGTSVSHLRKVPDKWITISGFOIEETIDRETSGNLEQLLAVKSI RS 246
DB 194 RGTDEMKPTITLCTRSATHLRVEEYKANKSIEDISKETHGSLAEALTVYKQCN 253
QY 247 IPAYIAETLYYAMKAGTGDHLLIRVWVSREIDLFNIRKEFRKNFATSLYMIKDTSG 306
DB 254 LHSYFAERLYYAMKAGTRDGLIRNIYSRSEIDLNLKHPKMYGKTLSSMIMEDTSG 313
QY 307 DYKKAALLLCGED 319
DB 314 DYKKAALLSLVGS 326

RESULT 23
ANX3 HUMAN
ID ANX3 HUMAN STANDARD; PRT; 323 AA.
AC P124329;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant
DE protein III) (PAP-III) (35-alpha calcimedlin) (Inositol 1,2-cyclic
DE phosphate 2-phosphohydrolase).
GN ANX3 OR ANX3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88273202; PubMed=2968983;
RA Pedinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K.,
RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.-S.,
RA Pratt D., Wachtel L., Hession C., Frey A.Z., Wallner B.P.;
RT "Five distinct calcium and phospholipid binding proteins share
RT homology with lipocortin I.";
RL J. Biol. Chem. 263:10799-10811(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91301701; PubMed=1830024;
RA Tait J.F., Frankenberg D.A., Miao C.H., Killary A.M., Adler D.A.,
RA Dische C.M.;
RT "Chromosomal localization of the human annexin III (ANX3) gene.";
RL Genomics 10:441-448(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94102764; PubMed=8276419;
RA Tait J.F., Smith C., Xu L., Cookson B.T.;
RT "Structure and polymorphisms of the human annexin III (ANX3) gene.";
RL Genomics 18:79-86(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feltgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Smetten C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spletton M., Soares M.B., Bonaldi M.F., Casavert T.L., Scheetz T.E,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mulhally S.J,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schmecher A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 41-102 AND 126-138.
RX MEDLINE=8918212; PubMed=2975506;
RA Ross T.S., Tait J.F., Majerus P.W.;
RT "Identity of inositol 1,2-cyclic phosphate 2-phosphohydrolase with
RT lipocortin III.";
RL Science 248:605-607(1990).
RN [6]
RP SEQUENCE OF 41-79; 85-88; 104-119; 126-150 AND 217-323.
RX MEDLINE=8918212; PubMed=2975506;
RA Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
RA Hendrickson L.E., Fujikawa K.;
RT "Placental anticoagulant proteins: isolation and comparative
RT characterization four members of the lipocortin family.";
RL Biochemistry 27:6268-6276(1988).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=96229894; PubMed=8639653;
RA Favier-Perron B., Lewit-Bentley A., Russo-Marie F.;

RT "The high-resolution crystal structure of human annexin III shows
 RT subtle differences with annexin V." ;
 RL Biochemistry 35:1740-1744(1996).
 RN [8]
 RP VARIANTS ASN-19; ASN-219; LEU-251 AND SER-291.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes." ;
 RL Nat. Genet. 22:231-238(1999).
 RN [9]
 RP ERRATUM.
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373(1999).
 CC -1- FUNCTION: Inhibitor of phospholipase A2, also possesses anti-
 CC coagulant properties. Also cleaves the cyclic bond of inositol
 CC 1,2-cyclic phosphate to form inositol 1-phosphate.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; M20560; AAA59496.1; -;
 DR EMBL; M63310; AAA52284.1; -;
 DR EMBL; L20591; AAA16713.1; -;
 DR EMBL; BC000871; AAH00871.1; -;
 DR PIR; A47658; LHMU3.
 DR PDB; 1AXN; 08-MAR-96.
 DR PDB; 1A1I; 12-MAR-97.
 DR SWISS-2DPAGE; P12429; HUMAN.
 DR Aarhus/Ghent-2DPAGE; 5205; IEF.
 DR PMMA-2DPAGE; P12429; IEF.
 DR Genew; HGNC:541; ANXA3.
 DR MIM; 106490; -;
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PFO0191; annexin; 4.
 DR PRINTS; PRO0196; ANNEXIN.
 DR PRODOM; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat;
 KW Phospholipase A2 inhibitor; 3D-structure; Polymorphism.
 FT REPEAT 27 87 ANNEXIN 1.
 FT REPEAT 99 159 ANNEXIN 2.
 FT REPEAT 183 243 ANNEXIN 3.
 FT REPEAT 258 318 ANNEXIN 4.
 FT VARIANT 19 19 S -> N (in dbSNP:59511).
 FT /FTId=VAR_013914.
 FT I -> N (in dbSNP:5948).
 FT /FTId=VAR_013915.
 FT VARIANT 219 219 P -> L (in dbSNP:5549).
 FT /FTId=VAR_013916.
 FT VARIANT 251 251 F -> S (in dbSNP:5941).
 FT /FTId=VAR_013917.
 FT VARIANT 291 291 S -> G (in REF. 6).
 FT H -> R (in REF. 6).
 FT CONFLICT 146 146
 FT CONFLICT 294 294
 FT TURN 4 5
 FT TURN 16 17
 FT HELIX 20 31

FT HELIX 38 45
 FT TURN 46 47
 FT HELIX 50 64
 FT HELIX 68 75
 FT HELIX 78 88
 FT HELIX 91 103
 FT HELIX 110 119
 FT HELIX 122 136
 FT HELIX 140 147
 FT HELIX 150 160
 FT TURN 161 162
 FT HELIX 172 185
 FT TURN 186 188
 FT HELIX 194 203
 FT HELIX 206 220
 FT HELIX 224 231
 FT HELIX 234 262
 FT HELIX 269 279
 FT TURN 280 283
 FT HELIX 284 295
 FT HELIX 299 306
 FT HELIX 309 319
 SQ SEQUENCE 323 AA; 36375 MW; 4128C715491FC132 CRC64;
 Query Match 50.7%; Score 811; DB 1; Length 323;
 Best Local Similarity 50.2%; Pred. No. 9.7e-46;
 Matches 158; Conservative 61; Mismatches 96; Indels 0; Gaps 0;
 QY 6 RGVTVDPFGDEBADAETLRKANKGLGTDEESITLTLTSKSNARQROISNAFPLFGRLD 65
 DB 9 RGVTRVDPSPSPVDAEAIQKAIKRGITGDEKMLISITLTSNARQROIVKVEYAAKGL 68
 QY 66 LIDLKSELGKPEKLIYALMKPSRLYDAYELKALKAGAGNTEKVLTEIIASRTPEELRAI 125
 DB 69 KDLKDDLSGHEFHLVAVLTPPAVDAKQKSKMGAGNEDALIELLTRSRQMKOI 128
 QY 126 KQYEEBEGSLLEDDVVGDTSGYQRMVYLLQANDPDAGIDEADEVDAQALFQAGEI 185
 DB 129 SQAYVTYVYKSLGDDISSETSGDFRKALITLADGRDESLKYDEHLAKQDAQLYVAGEN 188
 QY 186 KMGTDKEKFTITFGPVSVHLKVPKVMYTIISGFOEETITDETSNLEQLLAVVKSIR 245
 DB 189 KMGTDKEKFTETLCSPQKLTDEYRNISQKDIVSISKELSGHFEDLLAIIVCYR 248
 QY 246 S1PAYLAETLYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKPEPRKNFATSLYMKIGDS 305
 DB 249 NTPAPLAETLHAKLGIGTDEFTLNKRWVSSEIDLIRTEPKKHYGYSLYSAIKSDTS 308
 QY 306 GDYKALLDLGCEBD 320
 DB 309 GDYEITLTKICGDD 323
 RESULT 24
 ANX3 MOUSE
 ID ANX3 MOUSE STANDARD; PRT; 323 AA.
 AC 035639;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant
 DE protein III) (PAP-III) (35-alpha calcimedlin).
 GN ANXA3 OR ANX3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=98172733; PubMed=9511742;
 RA Fernandez M.P., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 RA Morgan R.O.;

"Mouse annexin III cDNA, genetic mapping and evolution."
 RL Gene 207:43-51(1998).
 CC - FUNCTION: Inhibitor of phospholipase A2, also possesses anti-coagulant properties.
 CC - DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC - SIMILARITY: Belongs to the annexin family.
 CC - SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 CC EMBL: AJ001633; CAA04887.1; -
 CC HSSP: P12429; IAXN.
 DR MGD; MG1:1201378; Anx3.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat;
 KW Phospholipase A2 inhibitor.
 FT REPEAT 27 87 ANNEXIN 1.
 FT REPEAT 99 159 ANNEXIN 2.
 FT REPEAT 183 243 ANNEXIN 3.
 FT REPEAT 258 318 ANNEXIN 4.
 FT REPEAT 323 AA; 36371 MW; A1890255953750 CRC64;
 SQ SEQUENCE 323 AA; 50.6%; Score 809; DB 1; Length 323;
 Query Match Best Local Similarity 49.8%; Pred. No. 1.3e-45; Mismatches 97; Indels 0; Gaps 0;
 Matches 157; Conservative 61; Mismatches 97; Indels 0; Gaps 0;
 QY 6 RGTWDPGPFDERADAETLRKAMKGLTDEESILTLTSSNAQROETISAAFKTLFGRL 65
 DB 9 RGTWDPGPFSPSDAERAIKATIGTDEKTLINILTERNAQROLIVKQYQAYGCEL 68
 QY 66 LDDKSELTKFEKLIYALMKPSRLYDAVELKHALKAGTNEKVLTEIIASRTBELRAI 125
 DB 69 KDLKGLDLSGHFHVWVALYAPALPDANELKSMKGTGDEDLIELITRTRSRQMKEI 128
 QY 126 KQYEEYSGSLLEDVVGDTSGYQKMLVLLQANRPDAGIDAEQVQDQALFOGEL 185
 DB 129 SQAYVTYKKSGLDIDSETSGDFRKALLTLADGRDLSLVDEHLAKDQOTLYNAGE 188
 QY 186 KWTGDEDEKFTITFGTRSVSHLRKVPDKYMTISGQIEETIDRETSGNLEOLLAVKSKIR 245
 DB 189 KWTGDEDEKFTIEVLCLRSFPQKLTFFDEYRNISQKDIEDISIGELSGHEDLLAVHAR 248
 QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFIIRKFRKNAFTSLYSMTKGDTS 305
 DB 249 NTPAFLEARLHQALKGAGTDEFTLRINWVSSEIDLDIRHFKHGYGSLYSALQSDTS 308
 QY 306 GDYKALLLLCGEDD 320
 DB 309 GDYRTVLLKICGEDD 323
 RESULT 25
 ANX3 RAT STANDARD; PRT; 324 AA.
 ID ANX3 RAT
 AC P14669;
 DT 01-APR-1990 (rel. 14, Created)
 DT 01-APR-1990 (rel. 14, Last sequence update)
 DT 10-OCT-2003 (rel. 42, Last annotation update)
 DE Annexin A3 (Annexin III) (lipocortin II) (placental anticoagulant protein III) (PAP-III) (35-alpha calcimedlin).
 DE ANX3 OR ANX3.

Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A. Pubmed=296983;
 RX MEDLINE=88273202; Medline=296983;
 RA Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K.,
 RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
 RA Pratt D., Wachtel L., Hession C., Frey A.Z., Wallner B.P.;
 RA "Five distinct calcium and phospholipid binding proteins share
 RT homology with lipocortin I."
 RL J. Biol. Chem. 263:10799-10811(1988).
 CC - FUNCTION: Inhibitor of phospholipase A2, also possesses anti-coagulant properties.
 CC - DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC - SIMILARITY: Belongs to the annexin family.
 CC - SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 CC EMBL: M20559; AAA41511.1; -
 CC HSSP: P12429; IAXN.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat;
 KW Phospholipase A2 inhibitor.
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 324 AA; 36322 MW; 5BAC2BAEB2AE47 CRC64;
 SQ SEQUENCE 324 AA; 48.8%; Score 781; DB 1; Length 324;
 Query Match Best Local Similarity 48.8%; Pred. No. 8.5e-44; Mismatches 99; Indels 0; Gaps 0;
 Matches 152; Conservative 64; Mismatches 99; Indels 0; Gaps 0;
 QY 6 RGTWDPGPFDERADAETLRKAMKGLTDEESILTLTSSNAQROETISAAFKTLFGRL 65
 DB 10 RGTNNYGFNPSPSDAERAIKATIGTDEKTLINILTERNAQROLIVKHICAYEAC 68
 QY 66 LDDKSELTKFEKLIYALMKPSRLYDAVELKHALKAGTNEKVLTEIIASRTBELRAI 125
 DB 70 KADLKGDLSGHFHVWVALYAPAVPAKQKSMRGKTGDEDTLIELITRTRSRQMKEI 128
 QY 126 KQYEEYSGSLLEDVVGDTSGYQKMLVLLQANRPDAGIDAEQVQDQALFOGEL 185
 DB 130 SQAYVTYKKNLRDIDSETSGDFRKALLTLADGRDLSLVDEHLAKDQOTLYNAGE 188
 QY 186 KWTGDEDEKFTITFGTRSVSHLRKVPDKYMTISGQIEETIDRETSGNLEOLLAVKSKIR 245
 DB 190 KWTGDEDEKFTIEVLCLRSFPQKLTFFDEYRNISQKDIEDISIGELSGHEDLLAVHAR 248
 QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFIIRKFRKNAFTSLYSMTKGDTS 305
 DB 250 NTPAFLEARLHQALKGAGTDEFTLRINWVSSEIDLDIRHFKHGYGSLYSALQSDTS 308
 QY 306 GDYKALLLLCGEDD 320
 DB 310 GDYRTVLLKICGEDD 324

Db 121 ELFAIKQVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRPDPAGIDEEQVEDQALF 180
181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKWTTISGFOIETITDETSQNLQOLLAV 240
Qy 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKWTTISGFOIETITDETSQNLQOLLAV 240
Db 241 VKSIRSTPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKNFATSLYSMI 300
Qy 241 VKSIRSTPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKNFATSLYSMI 300
Db 301 KGDTSGDYKKALLLLCGEDD 320
Qy 301 KGDTSGDYKKALLLLCGEDD 320
Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 2

S27214
anexin V - bovine
N:Alternate names: Cabp33; Cabp37
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C:Accession: S27214; S27215
R:Leamont, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Giambanco, I.; Bi
Biochim. Biophys. Acta 1160, 76-83, 1992
A:Title: Novel isoforms of Cabp 33/37 (Anexin V) from mammalian brain: structural and p
A:Reference number: S27214; MUID:93041974; PMID:1420335
A:Accession: S27214
A:Molecule type: protein
A:Residues: 1-320 <LEA>
A:Accession: S27215
A:Molecule type: protein
A:Residues: 1-35,'T',37-124,'E',126-320 <LE2>
A:Note: It is uncertain whether the sequence differences are due to allelic variation or
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
derstood.
C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula
olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin
F:17-88/Domain: annexin repeat homology <AX1>
F:28-44/Region: endonexin fold #status predicted
F:89-160/Domain: endonexin repeat homology <AX2>
F:100-116/Region: endonexin repeat homology <AX3>
F:172-244/Domain: annexin repeat homology <AX4>
F:184-200/Region: endonexin fold #status predicted
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin fold #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:22/Binding site: phosphate (Thr) (covalent) #status experimental
F:27,29,31,71/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) #status predicte
F:32,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F:72,77/Binding site: calcium, low affinity (Leu, Gly, Asp) #status predicte
F:99,101,103,143/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status pred
F:258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status pred

Query Match 96.6%; Score 1545.5; DB 1; Length 320;
Best Local Similarity 96.9%; Pred. No. 1.2e-92;
Matches 310; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 2 AOVLRGTVDPEPGDERADAEFLRKAMKGLGTDEESILTLTSSNAQROGISAFFTLF 61
Db 1 AOVLRGTVDPEPGDERADAEFLRKAMKGLGTDEESILTLTSSNAQROGISAFFTLF 60
Qy 62 GRDLIDDLKSELTKGFEKLYVALMKPSRLYAYELKHALKGAGTNEKYLTEIIASRTPEE 121
Db 61 GRDLIDDLKSELTKGFEKLYVALMKPSRLYAYELKHALKGAGTNEKYLTEIIASRTPEE 120
Qy 122 LRAIKQVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRPDPAGIDEEQVEDQALFQ 181
Db 121 LRAIKQVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRPDPAGIDEEQVEDQALFQ 180
Qy 182 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKWTTISGFOIETITDETSQNLQOLLAV 241

Db 181 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKWTTISGFOIETITDETSQNLQOLLAV
Qy 242 KSIIRSTPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKNFATSLYSMI
Db 241 KSIIRSTPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKNFATSLYSMI
Qy 302 GDTSGDYKKALLLLCGEDD 320
Db 301 GDTSGDYKKALLLLCGEDD 320

RESULT 3

LUR75
anexin V - rat
N:Alternate names: endonexin II; lipocortin V; placental anticoagulant pr
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-19
C:Accession: C29250; S66680
R:Pepinsky, R.B.; Tizard, R.; Matallano, R.J.; Sinclair, L.K.; Miller, G
J. Biol. Chem. 263, 10799-10811, 1988
A:Title: Five distinct calcium and phospholipid binding proteins share ho
A:Reference number: A92659; MUID:88273202; PMID:2968983
A:Accession: C29250
A:Molecule type: mRNA
A:Residues: 1-319 <PEP>
A:Cross-references: GB:M21730; NID:G205138; PID:AAA41512.1; PID:G205139
R:Imai, Y.; Kohsaka, S.
Eur. J. Biochem. 232, 327-334, 1995
A:Title: Structure of rat annexin V gene and molecular diversity of its t
A:Reference number: S66680; MUID:96035863; PMID:7556178
A:Accession: S66680
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-319 <IMA>
A:Cross-references: EMBL:D42136
C:Comment: Annexin V has been proposed to play a role in the inhibition of
olipid-binding rather than proteolytic inactivation. It does not affect t
derstood.
C:Comment: Annexin V has been proposed to play a role in the inhibition of
olipid-binding rather than proteolytic inactivation. It does not affect t
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: calcium binding; duplication; endonexin fold; membrane-associ
F:2-319/Product: annexin V #status predicted <MAT>
F:16-87/Domain: annexin repeat homology <AX1>
F:27-43/Region: endonexin fold #status predicted
F:88-159/Domain: annexin repeat homology <AX2>
F:99-115/Region: endonexin repeat homology <AX3>
F:171-243/Domain: annexin repeat homology <AX4>
F:183-199/Region: endonexin fold #status predicted
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: endonexin fold #status predicted
F:26,28,30,70/Binding site: calcium, high affinity (Met, Gly, Gly, Glu)
F:31,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status p
F:71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F:98,100,102,142/Binding site: calcium, high affinity (Leu, Gly, Gly, As
F:257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Gly, A

Query Match 91.5%; Score 1464.5; DB 1; Length 319;
Best Local Similarity 92.1%; Pred. No. 2e-87;
Matches 292; Conservative 12; Mismatches 12; Indels 1; Gap

Qy 5 LRGTVDDPEPGDERADAEFLRKAMKGLGTDEESILTLTSSNAQROGISAFFTLF 61
Db 3 LRGTVDDPEPGDERADAEFLRKAMKGLGTDEESILTLTSSNAQROGISAFFTLF 60
Qy 65 LLDLIDDLKSELTKGFEKLYVALMKPSRLYAYELKHALKGAGTNEKYLTEIIASRTPEE 121
Db 63 LLDLIDDLKSELTKGFEKLYVALMKPSRLYAYELKHALKGAGTNEKYLTEIIASRTPEE 120
Qy 125 IKQVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRPDPAGIDEEQVEDQALFQ 181
Db 125 IKQVEEYEGSSLEDVVGDTSGYQRMVLVLLQANRPDPAGIDEEQVEDQALFQ 180

Db 123 IKQAVEEYSGNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAQVELDQAALFQAGE 182

Qy 185 LKMGDEEFTITITFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSNGLLEQLLAVVSI 244

Db 183 LKMGDEEFTITITFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSNGLLEQLLAVVSI 242

Qy 245 RSIPAYLAETLYYAMKAGAGTDHDLIRVWVSSEIDLFINRKEFRKPFATSLYSIKGDT 304

Db 243 RSIPAYLAETLYYAMKAGAGTDHDLIRVWVSSEIDLFINRKEFRKPFATSLYSIKGDT 302

Qy 305 SGDYKKALLILIC-GEED 320

Db 303 SGDYKKALLILICGEED 319

RESULT 4

LUCBS

annexin V - chicken

N/Alternate names: anchorin CII; endonexin II; lipocortin V; placental anticoagulant pro

C/Species: Gallus gallus (chicken)

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000

C/Accession: A35381; A28623; B40404; S32523; S08771

R/Fernandez, M.P.; Selamin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.; Mc

J. Biol. Chem. 265, 8344, 1990

A/Reference number: A35381; MUID:90243721; PMID:2159478

A/Contents: erratum

A/Accession: A35381

A/Molecule type: mRNA

A/Residues: 1-321 <FER>

A/Cross-references: GB:M30971; GB:J03194; NID:G211138; PIDN:AAA48591.1; PID:G211139

R/Fernandez, M.P.; Selamin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.; Mc

J. Biol. Chem. 263, 5921-5925, 1988

A/Title: The structure of anchorin CII, a collagen binding protein isolated from chondro

A/Reference number: A28623; MUID:88186917; PMID:2893522

A/Accession: A28623

A/Molecule type: mRNA

A/Residues: 1-116; LKCRILRNQVEYANLGRNKITGRHQAIFRDCWSSCGQRIET, 163-167, 'R', 169-321 <

R/Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.

J. Biol. Chem. 266, 10678-10685, 1991

A/Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective particl

A/Reference number: A40404; MUID:91244852; PMID:2037607

A/Accession: B40404

A/Molecule type: protein

A/Residues: 188-199 <GRN>

A/Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched micros

R/Boutead, C.M.; Brown, R.; Walker, J.H.

Biochem. J. 291, 601-608, 1993

A/Title: Isolation, characterization and localization of annexin V from chicken liver.

A/Reference number: S32523; MUID:93249384; PMID:8484740

A/Accession: S32523

A/Status: preliminary

A/Molecule type: protein

A/Residues: 6-20;85,'X',87-88,'X',90-93,'X',95-96,'XX',99-100,'X',102-103,'XX',106-107;1

C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

deretocod.

C/Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula

olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende

C/Superfamily: annexin I; annexin repeat homology <AX2>

C/Keywords: calcium binding; collagen binding; duplication; endonexin fold; membrane-ass

F/2-321/Product: annexin V #status predicted <MAT>

F/18-89/Domain: annexin repeat homology <AX1>

F/29-45/Region: endonexin fold #status predicted

F/90-161/Domain: annexin repeat homology <AX2>

F/101-117/Region: endonexin fold #status predicted

F/173-245/Domain: annexin repeat homology <AX3>

F/185-201/Region: endonexin repeat homology <AX3>

F/249-320/Domain: annexin repeat homology <AX4>

F/260-276/Region: endonexin fold #status predicted

F/260-276/Region: endonexin fold #status predicted

F/323-353/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) #status predicted

F/73-78/Binding site: calcium, low affinity (Ileu, Glu) #status predicted

F/100,102,104,144/Binding site: calcium, high affinity (Ile, Gly, Gly, Glu) #status pred

F/259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status pre

Query Match 80.6%; Score 1289; DB 1; Length 321;

Best Local Similarity 78.4%; Pred. No. 4.3e-76;

Matches 251; Conservative 38; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MAQVLRRTVDFPFQEDRAAETLRKAMKGLGDEESILLLTSRSNAQOEISAARCTL 60

Db 1 MAKYTRGTVAFSPFDPADAEALRKAMKMGDEEITILKITSRRNNAQOEIASAEKTL 60

Qy 61 FGRDLDDLKSELGTGKEKLIIVALKMPSRLYDAVEIKHALKGATNKVLTETIASTPE 120

Db 61 FGRDLVDDLKSELGTGKEETLMSLRPARIFDHALKHALKGATNEKVLTEIATSTPA 120

Qy 121 ELRAIKQVEEYSGSLEDVVDGTSYQRMVLVLLQANRPDPAIDEAQVELDQAALF 180

Db 121 EVGNIKQVWQVEYANIEDKITGETSGHPRLLVLLQANRPDGRVDEALVEKDAQLF 180

Qy 181 QAGELKMGDEEFTITFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSNGLLEQLLAV 240

Db 181 RAGELKMGDEEFTITFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSNGLLEQLLAV 240

Qy 241 VKSIRSIPIAYLAETLYYAMKAGAGTDHDLIRVWVSSEIDLFINRKEFRKPFATSLYSMT 300

Db 241 VKCIRSVPAFAETLYYAMKAGAGTDHDLIRVWVSSEIDLIRHFRKPFATSLYSMT 300

Qy 301 KQDTSQDYKKALLILICGEED 320

Db 301 QKDTSGDYKKALLILICGEED 320

RESULT 5

annexin VI - mouse

N/Alternate names: calcium-binding protein p68; calelectrin; calpobindin II

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C/Accession: S01786

R/Moss, S.E.; Crumpton, M.R.; Crumpton, M.J.

Eur. J. Biochem. 177, 21-27, 1988

A/Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family

A/Reference number: S01786; MUID:89030687; PMID:2972541

A/Accession: S01786

A/Molecule type: mRNA

A/Residues: 1-673 <MO>

A/Cross-references: EMBL:X13460; NID:953580; PIDN:CAA31808.1; PID:953581

A/Note: The authors translated the codon GCC for residue 329 as Gly

C/Comment: This abundant cytosolic protein binds to the inner surface of the cell membra

C/Superfamily: annexin VI; annexin repeat homology

C/Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosphol

F/2-673/Product: annexin VI #status predicted <MAT>

F/23-94/Domain: annexin repeat homology <AX1>

F/34-50/Region: endonexin fold #status predicted

F/95-166/Domain: annexin repeat homology <AX2>

F/106-122/Region: endonexin fold #status predicted

F/178-250/Domain: annexin repeat homology <AX3>

F/190-206/Region: endonexin fold #status predicted

F/254-325/Domain: annexin repeat homology <AX4>

F/265-281/Region: endonexin repeat homology <AX4>

F/366-437/Domain: annexin repeat homology <AX5>

F/377-393/Region: endonexin fold #status predicted

F/438-509/Domain: annexin repeat homology <AX6>

F/449-466/Region: endonexin fold #status predicted

F/527-598/Domain: annexin repeat homology <AX7>

F/538-554/Region: endonexin fold #status predicted

F/602-673/Domain: annexin repeat homology <AX8>

F/613-629/Region: endonexin fold #status predicted

F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 58.9%; Score 942; DB 1; Length 673;

Best Local Similarity 59.4%; Pred. No. 2.7e-53;

Matches 187; Conservative 49; Mismatches 79; Indels 0; Gaps 0;

Query Match 58.2%; Score 931; DB 1; Length 318;
 Best Local Similarity 58.9%; Pred. No. 5.4e-53;
 Matches 185; Conservative 51; Mismatches 78; Indels 0; Gaps 0;

QY 7 GTVDPFGPDERADAEITLRKMKGLGTDDEEILTLTSSRAQOEISAAKTLFGDRL 66
 DB 5 GTVAAAGGFAAEADQITLRKMKGLGTDDEAIIISLVYRSTAOEIRTAVKSTIGDRL 64
 QY 67 DDLKSELTKREKLIIVALKMSPRLYDAVELKHALKGAGTNEKVLTIIASIPPELAIK 126
 DB 65 DDLKSELISGNPEQYIILGMPITVYDQELRAKMGAGTDEGCIIEILASIPPEIRIN 124
 QY 127 QVVEEYEGSSLEDVVDGTSYGYORMLVLLQANRDPDAGIDEAQVEQDAQALFOAGELK 186
 DB 125 QTVQLOQGRSLEDIRDSDTSPMFORVLVLSAGRDENYIDDLVADQADLYEAGEKK 184
 QY 187 WGTDEEFITITGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVKSI 246
 DB 185 WGTDEVAFELTVLCGRNNHLLHVFDEYKRISQKQIEOSISSETSGSFEDLLAIVKCMRN 244
 QY 247 IPAYLAETLYYKMGAGTDHTLIRVWVSRSSEIDLFINRKEFRKNFATSLYMIKADTSG 306
 DB 245 KSAVFAERLYKMKGLGTDNDTLIRVWVSRAEIDMMDIRANFKRLYKSLYSFICKDTSG 304
 QY 307 DYKALLLLCGEDD 320
 DB 305 DYKALLLLCGDD 318

RESULT 8

annexin VI - rat
 S52844
 N:Alternate names: calcium-binding protein 65/67
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S65683; S52844
 R:Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W.
 Eur. J. Biochem. 230, 741-751, 1995
 A:Title: cDNA cloning and tissue-specific regulation of expression of rat calcium-binding protein 65/67
 A:Reference number: S65683; MUID:95313133; PMID:7607247
 A:Accession: S65683
 A:Molecule type: mRNA
 A:Residues: 1-673 <FAN>
 A:Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181
 A:Experimental source: liver
 C:Superfamily: annexin VI; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associated protein
 F:12-673/Product: annexin VI #status predicted <MAT>
 F:134-94/Region: annexin repeat homology <AX1>
 F:106-166/Region: endonexin fold #status predicted
 F:106-122/Region: annexin repeat homology <AX2>
 F:1178-250/Domain: endonexin fold #status predicted
 F:190-206/Region: endonexin fold #status predicted
 F:254-325/Domain: annexin repeat homology <AX4>
 F:265-281/Region: endonexin fold #status predicted
 F:365-437/Domain: annexin repeat homology <AX5>
 F:377-393/Region: endonexin fold #status predicted
 F:438-509/Domain: annexin repeat homology <AX6>
 F:449-465/Region: endonexin fold #status predicted
 F:527-598/Domain: annexin repeat homology <AX7>
 F:538-554/Region: endonexin fold #status predicted
 F:602-673/Domain: endonexin repeat homology <AX8>
 F:613-629/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 58.2%; Score 931; DB 1; Length 673;
 Best Local Similarity 59.0%; Pred. No. 1.4e-52;
 Matches 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;

QY 6 RGTVDPFGPDERADAEITLRKMKGLGTDDEEILTLTSSRAQOEISAAKTLFGDRL 65
 DB 5 GTVAAAGGFAAEADQITLRKMKGLGTDDEAIIISLVYRSTAOEIRTAVKSTIGDRL 64

DB 11 RGSVHDEPADPDANQADAEALTYAMKFGSDKESILELITSSNNKQOEICQSYSLYKGLD 70
 QY 66 LDDLKSELTKREKLIIVALKMSPRLYDAVELKHALKGAGTNEKVLTIIASIPPELAIK 125
 DB 71 IADLTKELTKREKLIIVALKMSPRLYDAVELKHALKGAGTNEKVLTIIASIPPELAIK 125
 QY 126 KOVVEEYEGSSLEDVVDGTSYGYORMLVLLQANRDPDAGIDEAQVEQDAQALFOAGELK 185
 DB 131 VAAKQAEYEDLSDIIGDTSYGYORMLVLLQANRDPDAGIDEAQVEQDAQALFOAGELK 190
 QY 186 KMGTDKEFTITGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVKSI 245
 DB 191 KMGTDKEFTITGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVKSI 245
 QY 246 SIPAYLAETLYYKMGAGTDHTLIRVWVSRSSEIDLFINRKEFRKNFATSLYMIKADTSG 305
 DB 251 STEYFAERLYKMKGLGTDNDTLIRVWVSRAEIDMMDIRANFKRLYKSLYSFICKDTSG 310
 QY 306 GDYKALLLLCGEDD 320
 DB 311 GEYKALLLLCGDD 325

RESULT 9

annexin VI [validated] - human
 S52844
 N:Alternate names: calcium-binding protein, 68k; calelectrin; calphobindin II
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
 C:Accession: U00032; S00263; S18519; A31079; JX0091; B34459; B31953; A53507
 R:Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; Sh
 J. Biochem. 106, 43-49, 1989
 A:Title: Structure and expression of cDNA for calphobindin II, a human placental coagula
 A:Reference number: U00032; MUID:89380132; PMID:2528541
 A:Accession: U00032
 A:Molecule type: mRNA
 A:Residues: 1-673 <IWA>
 A:Cross-references: EMBL:D00510; NID:g219550; PIDN:BA00400.1; PID:g219551
 R:Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crompton, M.J.
 EMBO J. 7, 21-27, 1988
 A:Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p68:
 A:Reference number: S00263; MUID:88196081; PMID:3258820
 A:Accession: S00263
 A:Molecule type: mRNA
 A:Residues: 1-618, 'D', 620-673 <CRI>
 A:Cross-references: EMBL:Y00097; NID:g35217; PIDN:CAA68286.1; PID:g35218
 A:Accession: S18519
 A:Molecule type: protein
 A:Residues: 103-113; 167-172, 'X', 174-177; 232-235, 'F', 237-240; 251-258; 277-281; 359-362, 'G',
 A:Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-Glu
 A:Note: eight calcium ions are bound in the presence of phospholipid
 R:Suedhof, T.C.; Slaughter, C.A.; Leznicki, I.; Barjon, P.; Reynolds, G.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988
 A:Title: Human 67-kDa calelectrin contains a duplication of four repeats found in 35-kDa
 A:Reference number: A31079; MUID:88124902; PMID:2963335
 A:Accession: A31079
 A:Molecule type: mRNA
 A:Residues: 1-225, 'MK', 228-554, 'T', 556-673 <SUB>
 A:Cross-references: GB:U03578; NID:g179975; PIDN:AAA35656.1; PID:g179976
 R:Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; Sh
 J. Biochem. 107, 43-50, 1990
 A:Title: Structure and properties of calphobindin II, an anticoagulant protein from huma
 A:Reference number: JX0091; MUID:90236978; PMID:2139657
 A:Accession: JX0091
 A:Molecule type: protein
 A:Residues: 2-299; 307-314; 320-445; 447-549; 581-673 <YOS>
 R:Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T.
 J. Biol. Chem. 264, 17222-17230, 1989
 A:Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding protein
 A:Reference number: A34459; MUID:90008880; PMID:2529258
 A:Accession: B34459
 A:Molecule type: protein
 A:Residues: 10-25; 69-75; 136-151; 192-207; 209-220; 300-306 <HAY>

A:Experimental source: placenta
 R:Ahm, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
 J. Biol. Chem. 263, 18657-18663, 1988
 A>Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2
 inhibitor.
 A:Reference number: A92696; MUID:89066652; PMID:2974032
 A:Accession: B31953
 A:Molecule type: protein
 A:Residues: 90-108, 'L', 110-126, 127, 265-276, 286-302, 626-654 <AHN>
 R:Hyatt, S.U.; Liao, L.; Chapline, C.; Jaken, S.
 Biochemistry 33, 1223-1228, 1994
 A>Title: Identification and characterization of alpha-protein kinase C binding proteins
 A:Reference number: A53507; MUID:94153907; PMID:8110754
 A:Accession: A53507
 A:Molecule type: protein
 A:Residues: 'X', 473-480, 'DY' <HYA>
 C:Comment: This abundant cytosolic protein binds to the inner surface of the cell membrane
 C:Genetics:
 A:Gene: GDB:ANX6
 A:Cross-references: GDB:119681; OMIM:114070
 A:Map position: 5q32-5q34
 C:Superfamily: annexin VI; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosphol
 F:2-673/Product: annexin VI #status experimental <MAT>
 F:23-94/Domain: annexin repeat homology <AX1>
 F:34-50/Region: endonexin fold #status predicted
 F:106-122/Region: endonexin repeat homology <AX2>
 F:190-206/Region: endonexin repeat homology <AX3>
 F:178-250/Domain: annexin repeat homology <AX3>
 F:190-206/Region: endonexin fold #status predicted
 F:254-325/Domain: annexin repeat homology <AX4>
 F:265-281/Region: endonexin repeat homology <AX5>
 F:365-437/Domain: annexin repeat homology <AX5>
 F:377-393/Region: endonexin fold #status predicted
 F:438-509/Domain: annexin repeat homology <AX6>
 F:449-465/Region: endonexin fold #status predicted
 F:527-598/Domain: annexin repeat homology <AX7>
 F:538-554/Region: endonexin fold #status predicted
 F:602-673/Domain: annexin repeat homology <AX8>
 F:613-629/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 57.8%; Score 927; DB 1; Length 673;
 Best Local Similarity 57.8%; Pred. No. 2.5e-52;
 Matches 182; Conservative 52; Mismatches 81; Indels 0; Gaps 0;

6 RGTWDPFGPDERADAEFLRKAMKGLGDEESITLLTSRNSAORQETISAFTLFGRLD 65
 11 RGSITHDPFGDPNDADALVTAMKPGSDKEALIDITSRNROQEVCSYKSLYKDL 70
 QY 66 LDDKSELTKGFEKLVALKMPSRLYDAVELKHALKGAQTEKVLTEIISARTPEELRAI 125
 Db 71 IADLKVELTKGFEFLVGLMPPAYCDAKEIKDAISGIGTDEKCLIELASRTPEEQHQL 130
 QY 126 KQVEEYSGSLEDVVDGTSYGYQRMVTLQANRPDAGIDEAQNVDQADALFOAGEL 185
 Db 131 VAAKYDAVERDLIEDITDTSYGFQKMLVLLQGTREDDVASELVQODVQDYAEAE 190
 QY 186 KMGTEDEKFTITFGRSVSHLRKYVDKMTTSGFOIEETIDETSQNLQOLLAVVKSIR 245
 Db 191 KMGTEDEAFITILGRSKQHLNLFDEVLTKTKGRTKESISGELSGDEKMLAVKQIR 250
 QY 246 SIPAVIAETLYYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKNFATSLYSMTKGDTS 305
 Db 251 STPEYFAERLFRAMKGLGTRNTLIRIVWSRELMDLRIETFRYKESLSYMTKNDTS 310
 QY 306 GDYKKALLLCCGEDD 320
 Db 311 GEYKTKLLKLSGGDD 325

RESULT 10
 LUBO4

annexin IV - bovine
 N:Alternate names: 33k calelectrin; chromobindin IV; endonexin; lipocortin
 C:Species: Bos primigenius taurus (cattle)
 C:Update: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-19
 C:Accession: A1578; D45066; S59624; A45066; B45066; C45066; G450
 R:Hamman, H.C.; Gaffey, L.C.; Lynch, K.R.; Creutz, C.E.
 Biochem. Biophys. Res. Commun. 156, 660-667, 1988
 A>Title: Cloning and characterization of a cDNA encoding bovine endonexin
 A:Reference number: A1578; MUID:89050088; PMID:2847715
 A:Accession: A1578
 A:Molecule type: mRNA
 A:Residues: 1-319 <HAM>
 A:Cross-references: GB:X13627; NID:9215; PIDN:CA31954.1; PID:9216; GB:M2
 R:Kojima, K.; Ogawa, H.K.; Sano, N.; Yamamoto, K.; Irimura, T.; Osawa, T
 J. Biol. Chem. 267, 20536-20539, 1992
 A>Title: Carboxylate-binding proteins in bovine kidney have consensus am
 A:Reference number: A45066; MUID:93015942; PMID:1400371
 A:Accession: D45066
 A:Molecule type: protein
 A:Residues: 10-18, 'X', 20-22, 'X', 24-25, 29-48, 101-107, 'X', 109-118, 'X', 194-1
 A:Experimental source: kidney
 A:Note: sequence extracted from NCBI backbone (NCBIP:116211, NCBIP:116208)
 A:Note: these fragments are derived from a 33k protein that exhibited Ca-
 A:Note: 12-Met and 12-Tyr were also found
 R:Sohma, H.; Matsushima, N.; Watanabe, T.; Hattori, A.; Kuroki, Y.; Akino
 Biochem. J. 312, 175-181, 1995
 A>Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A
 A:Reference number: S59624; MUID:96077142; PMID:7492310
 A:Accession: S59624
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 29-44/72-77/112-119/163-180/181-190/226-235 <SOH>
 C:Comment: Annexins undergo reversible, calcium-dependent binding to mem
 C:Superfamily: annexin I; annexin repeat homology
 C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein;
 F:2-319/Product: annexin IV #status predicted <MAT>
 F:17-88/Domain: annexin repeat homology <AX1>
 F:28-44/Region: endonexin fold #status predicted
 F:89-160/Domain: annexin repeat homology <AX2>
 F:100-116/Region: endonexin fold #status predicted
 F:112-244/Domain: annexin repeat homology <AX3>
 F:184-200/Region: endonexin fold #status predicted
 F:248-319/Domain: annexin repeat homology <AX4>
 F:259-275/Region: endonexin fold #status predicted
 F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #stat
 F:125/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 57.8%; Score 924; DB 1; Length 319;
 Best Local Similarity 58.3%; Pred. NO. 1.5e-53;
 Matches 183; Conservative 51; Mismatches 80; Indels 0; Gaps 0;

7 GTWDPFGPDERADAEFLRKAMKGLGDEESITLLTSRNSAORQETISAFTLFGRLD 65
 6 GTVPAASGFNAABDQTLRKAMKGLGDEDAIINVLAVRTAQOELRTAYKTTIGRD 70
 QY 66 LDDKSELTKGFEKLVALKMPSRLYDAVELKHALKGAQTEKVLTEIISARTPEELRAI 125
 Db 67 DDLKSELTKGFEKLVALKMPSRLYDAVELKHALKGAQTEKVLTEIISARTPEELRAI 125
 QY 127 KQVEEYSGSLEDVVDGTSYGYQRMVTLQANRPDAGIDEAQNVDQADALFOAGEL 185
 Db 126 QTYQLOGRSLEDVVDGTSYGFQKMLVLLQGTREDDVASELVQODVQDYAEAE 190
 QY 187 KMGTEDEKFTITFGRSVSHLRKYVDKMTTSGFOIEETIDETSQNLQOLLAVVKSIR 245
 Db 186 KMGTEDEKFTITFGRSVSHLRKYVDKMTTSGFOIEETIDETSQNLQOLLAVVKSIR 245
 QY 247 IPAVIAETLYYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKNFATSLYSMTKGDTS 305
 Db 246 KSAVFAERLFRAMKGLGTRNTLIRIVWSRELMDLRIETFRYKESLSYMTKNDTS 310
 QY 307 DYKALLLCCGEDD 320

A:Accession: S36136
 A:Molecule type: mRNA
 A:Residues: 1-77 <T02>
 A:Cross-references: EMBL:Z11742
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid vesicles.
 C:Genetics:
 A:Introns: 19/1; 58/2
 A>Note: The list of introns is incomplete
 C:Superfamily: annexin VII; annexin repeat homology
 C:Keywords: alternative splicing; calcium binding; duplication; endonexin fold; glycoprotein
 F:203-274/Domain: endonexin repeat homology <AX1>
 F:214-223/Region: endonexin fold #status predicted
 F:217-346/Domain: endonexin repeat homology <AX2>
 F:286-302/Region: endonexin fold #status predicted
 F:358-430/Domain: endonexin repeat homology <AX3>
 F:370-386/Region: endonexin fold #status predicted
 F:434-505/Domain: endonexin repeat homology <AX4>
 F:445-461/Region: endonexin fold #status predicted
 F:61.113/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.7%; Score 875; DB 1; Length 505;
 Best Local Similarity 55.2%; Pred. No. 3.9e-49;
 Matches 174; Conservative 58; Mismatches 83; Indels 0; Gaps 0;

QY 6 RGTVDPPGDERADAEATLRKAMKGLGTDDESILTLTSSNAQOEISAFTLFGRL 65
 DB 191 RGTITDASGFDPLRAEVLKAMKGGTDEQAIIIDCLGSRNKKOQOILSFTAYGKDL 250
 QY 66 LDDKSELTKGFEKLIIVALKPSRLYDAVELKALKGAGTNEKVLTEIIASRPEELRAI 125
 DB 251 IKDLKSELGNFEKTLTALMKTPIVLPDAVEIKKAIKAGTDEACLEIIASRNEHIREL 310
 QY 126 KOYEEBEGSSLEDDVVGTSYQRMVVLQANRPDAGIDEADEVODAOALFOAGEL 185
 DB 311 NRYKTEFFKKTLEEARSDTSRSHFQRLILSLSGNDBESTNVDMLVQDVQELVYAG 370
 QY 186 KMGTDSEKFTITGTRSVSHLRKVPKWTISGFQIEETIDRETSNQLQDLAVVKSIR 245
 DB 371 RLGTDESKFNAILCSRSRAHLVAVFNEYQMTGDIKRSICREMSGDLQGMALVAVCKL 430
 QY 246 SIPIVLAETLYYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKMFATSLYSMIKQDTS 305
 DB 431 NTPAFPAERLNKMRKAGTDRTLIRIMVSRSEIDLDIRAEVRYLYGKSLYHDITDTS 490
 QY 306 GDYKKAALLLCGEDD 320
 DB 491 GDYRKILLKTCGGND 505

RESULT 14
 LURB11
 N:Alternate names: calyculin-associated annexin protein CAP-50
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jun-2000
 C:Accession: JH0694; PH0950; A38250; PS0263
 R:Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 186: 1227-1235, 1992
 A:Title: Molecular cloning of rabbit CAP-50, a calyculin-associated annexin protein.
 A:Reference number: JH0694; MIMD:92378579; PMID:1380798
 A:Accession: JH0694
 A:Molecule type: mRNA
 A:Residues: 1-503 <T0K>
 A:Cross-references: DDBJ:D10883; NID:g471147; PIDN:BA01705.1; PID:g471148
 A:Experimental source: lung
 A:Accession: PH0950
 A:Molecule type: protein
 A:Residues: 104-141;213-231;254-262;270-280;285-309;319-337;429-448;478-492 <TK2>
 R:Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.
 J. Biol. Chem. 267: 8919-8924, 1992
 A:Title: A calyculin-associated protein is a newly identified member of the Ca(2+)/phosphatase family.
 A:Reference number: A38250; MIMD:92250478; PMID:1533622

A:Accession: A38250
 A:Molecule type: protein
 A:Residues: 104-141;213-223, 'X', 225-231;254-263;271-280;285-291, 'X', 293-309
 C:Comment: This protein binds specifically to calyculin in a Ca2+ dependent manner.
 C:Superfamily: annexin VII; annexin repeat homology
 C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phosphatase
 F:203-274/Domain: endonexin repeat homology <AX1>
 F:212-228/Region: endonexin fold #status predicted
 F:217-344/Domain: endonexin repeat homology <AX2>
 F:284-300/Region: endonexin fold #status predicted
 F:356-428/Domain: endonexin repeat homology <AX3>
 F:368-384/Region: endonexin fold #status predicted
 F:432-503/Domain: endonexin repeat homology <AX4>
 F:443-459/Region: endonexin fold #status predicted
 F:58/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.6%; Score 873; DB 1; Length 503;
 Best Local Similarity 54.6%; Pred. No. 5.2e-49;
 Matches 172; Conservative 60; Mismatches 83; Indels 0; Gaps 0;

QY 6 RGTVDPPGDERADAEATLRKAMKGLGTDDESILTLTSSNAQOEISAFTLFGRL 65
 DB 189 RGTITDASGFDPLRAEVLKAMKGGTDEQAIIIDCLGSRNKKOQOILSFTAYGKDL 250
 QY 66 LDDKSELTKGFEKLIIVALKPSRLYDAVELKALKGAGTNEKVLTEIIASRPEELRAI 125
 DB 249 IKDLKSELGNFEKTLTALMKTPIVLPDAVEIKKAIKAGTDEACLEIIASRNEHIREL 310
 QY 126 KOYEEBEGSSLEDDVVGTSYQRMVVLQANRPDAGIDEADEVODAOALFOAGEL 185
 DB 309 NRYKTEFFKKTLEEARSDTSRSHFQRLILSLSGNDBESTNVDMLVQDVQELVYAG 370
 QY 186 KMGTDSEKFTITGTRSVSHLRKVPKWTISGFQIEETIDRETSNQLQDLAVVKSIR 245
 DB 369 RLGTDESKFNAILCSRSRAHLVAVFNEYQMTGDIKRSICREMSGDLQGMALVAVCKL 430
 QY 246 SIPIVLAETLYYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKMFATSLYSMIKQDTS 305
 DB 429 NTPAFPAERLNKMRKAGTDRTLIRIMVSRSEIDLDIRAEVRYLYGKSLYHDITDTS 490
 QY 306 GDYKKAALLLCGEDD 320
 DB 489 GDYRKILLKTCGGND 503

RESULT 15
 A53152
 annexin XI - human
 C:Species: Homo sapiens (man)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 13-Aug-1995
 C:Accession: A53152
 R:Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; Van Venrooij, W.J.
 J. Biol. Chem. 269: 4240-4246, 1994
 A:Title: The 56K autoantigen is identical to human annexin XI.
 A:Reference number: A53152; MIMD:94140847; PMID:7508441
 A:Accession: A53152
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 1-505 <MIS>
 A:Cross-references: GB:L19605; NID:g457128; PIDN:AAA19734.1; PID:g457128
 C:Genetics:
 A:Gene: GDB:ANX11
 A:Cross-references: GDB:113076
 A:Map position: 9q41-q42
 C:Superfamily: annexin VII; annexin repeat homology
 C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein;
 F:203-274/Domain: endonexin repeat homology <AX1>
 F:275-346/Domain: endonexin repeat homology <AX2>
 F:358-430/Domain: endonexin repeat homology <AX3>
 F:434-505/Domain: endonexin repeat homology <AX4>

Query Match 54.1%; Score 865; DB 2; Length 505;
 Best Local Similarity 53.7%; Pred. No. 1.7e-48;

Query Match	50.7%;	Score 811;	DB 1;	Length 323;
Best Local Similarity	50.2%;	Pred. No. 3e-45;		
Matches 158;	Conservative 61;	Mismatches 96;	Indels 0;	Gaps 0;

RESULT 18

94-165/Domain: annexin repeat homology <AX3>
:105-121/Region: endonexin fold #status predicted
:177-249/Domain: annexin repeat homology <AX3>
:189-205/Region: endonexin fold #status predicted
:253-324/Domain: annexin repeat homology <AX4>
:264-280/Region: endonexin fold #status predicted
:20,219/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.1%; Score 785; DB 1; Length 324;
Best Local Similarity 48.3%; Pred. No. 1.5e-43;
Matches 152; Conservative 65; Mismatches 98; Indels 0; Gaps

Dbb 10 KGTINNYPGFNPESVDAAERKAIKIGTGDEKTLNITERSVAQRQLIVKOYEAVEQDA
Xy 6 RGTVPFGDFDERADAETLRKAMKGLGIDESILLLTSRSNAQOEISAFKTLFRGD
Xy :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Ddb 10 KGTINNYPGFNPESVDAAERKAIKIGTGDEKTLNITERSVAQRQLIVKOYEAVEQDA
Xy 66 LDDLKSELTGKEPEKLIALMKSRLYDAVELKHALKGAGTNEKVLTLEIASTPEELRA
Xy 70 KALLKQDLGSHEFHVAVLITAPAVFDAKOLKMSRGMGTEDDTLEILTITSQME
Ddb 126 KOYEERYSSLEDVDVGTSGYQMVLVLQANRPDAGIDEAQVEDQAALFOAG
Xy 130 SQAYATYAKKNLDDDISSESGPFRKALTLLADGGDSCLKYDEHLAKKDAGTLVDAG
Xy 186 KWGTDEKFTTTCGTSVSHLRKVPFKWMTISGFQJEFTIDETSGNLEBOLLAAVKS
Ddb 190 KWGTDEKFTTEICLRSPOLKLTPEBYRNISQKDIEDSLKGLSHPFDLLLAIVRC
Xy 246 SIPLVIAETLYVMKKGGTDHTLIRVMVSRSEIDLFNIRKERKKNPATSIYSMKGP
Ddb 250 NTFPLFLGRHQAOKGKGDEFTLNRIWRSRSELDLDIRREKKHYGCSLVASIQSD
Xy 306 GDYKCALLLCGEED 320
Ddb 310 GDYRTVLTKITCGSD 324

RESULT 19

LDB07
annexin VII, long form - human
N:Alternate names: synexin
N:Contains: annexin VII, long form; annexin VII, short form
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence revision 26-Jan-1996 #text_change 22-Jun-1
C:Accession: A54467; A32554; A39513; B39513
R:Shirvan, A.; Srivastava, M.; Wang, W.G.; Culttaro, C.; Magendzo, K.; M
Biochemistry 33, 6888-6901, 1994
A>Title: Divergent structure of the human synexin (annexin VII) gene and
A:Reference number: A54467; PMID:94264005; PMID:7515686
A:Accession: A54467
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Molecule type: mRNA
A:Residues: 1-468 <SHI>
R:Burns, A.L.; Magendzo, K.; Shirvan, A.; Srivastava, M.; Rojas, E.; All
Proc. Natl. Acad. Sci. U.S.A. 86, 3798-3802, 1989
A>Title: Calcium channel activity of purified human synexin and structun
A:Reference number: A32554; PMID:89264510; PMID:2542947
A:Accession: A32554
A:Molecule type: mRNA
A:Residues: 1-145,168-488 <BUR>
A:Cross-references: EMBL:J04543; NID:q338243; PIND:AAA3616.1; PID:q338
R:Magendzo, K.; Shirvan, A.; Culttaro, C.; Srivastava, M.; Pollard, H.B
U. Biol. Chem. 266, 3228-3232, 1991
A>Title: Alternative splicing of human synexin mRNA in brain, cardiac,
A:Reference number: A39513; PMID:91131630; PMID:1825209
A:Accession: A39513
A:Molecule type: mRNA
A:Residues: 137-145,168-176 <MAG>
A:Cross-references: EMBL:J05752
A:Accession: B39513
A:Molecule type: mRNA
A:Residues: 137-176 <MAG>
C:Comment: Annexins undergo reversible, calcium-dependent binding to me

deretocod.
C/Comment: The long form of annexin VII is more prevalent in brain, heart, and skeletal
C/Genetics:
A/Genes: GDB:ANX7
A/Cross-references: GDB:369042; OMIM:186360
A/Map position: 10q21.1-10q21.2
A/Intons: 17/3; 87/1; 124/1; 145/3; 167/3; 202/2; 233/3; 271/3; 328/3; 385/3; 411/1; 44
C/Superfamily: annexin VII; annexin repeat homology
C/Keywords: alternative splicing; calcium binding; calcium channel; duplication; endonex
F:1-488/Product: annexin VII, long form #status predicted <MFP>
F:1-145,166-488/Product: annexin VII, short form #status predicted <MA3>
F:188-259/Domain: annexin repeat homology <AX1>
F:199-215/Domain: annexin repeat homology <AX2>
F:260-331/Domain: annexin repeat homology <AX2>
F:271-287/Region: endonexin fold #status predicted
F:343-415/Domain: annexin repeat homology <AX3>
F:355-371/Region: endonexin fold #status predicted
F:419-488/Domain: annexin repeat homology <AX4>
F:430-446/Region: endonexin fold #status predicted

Query Match 48.8%; Score 780; DB 1; Length 488;
Best Local Similarity 48.1%; Pred. No. 5.1e-43;
Matches 153; Conservative 66; Mismatches 99; Indels 0; Gaps 0;

```
QY 1 MAQVLRGTVTDPPGPERADAEITLRKMGKLGTDSESLTLTSRNSAORQETSAAFKTL 60
DB 171 VTQVGTGTIRPANFPAIRDAEILRKMGKGFDEQAIYDVVNSNDROQIKKAFKTS 230
QY 61 FGRDLDDLKSELTEGFEKLIYALMKPSRLYAYELKHALKGAGTEKYLTIISARTPE 120
DB 231 YGKDLIKDKLSLGNMBELIALFMPPTYYDAMSLRKMGAGTERVLIILCTRITQ 290
QY 121 ELRAIKQVVEEBEGSSLEDDVVDGTSYYQRMVLVLLQANRPDAGIDEAQVEODAAQLF 180
DB 291 EIREIYRCQVSEFGRDLEKDIRSDTSGHFERLLVSCQGNRDNQINNMQAQEDQRLY 350
QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRETSGLLEQLLAV 240
DB 351 QAGEBGLGDESCFNMILATRSFPOLKATMEAYSRMARNDLSSVSREFSGIVESGLKTI 410
QY 241 VKSIRSIYAIYLAETLYYKMGAGTDHTLIRVMSRSEIDLINIKERKKNATSLYSMT 300
DB 411 LOCALNRPAFPAERLYYKMGAGTDSTLVRIVTRSEIDLVOIKOMFQOMYOKTLGTMTI 470
QY 301 KGDTSGDYKKAALLLCCGE 318
DB 471 AGDTSGDYRRLLLAIVGQ 488
```

RESULT 20

S29170

N:Alternate names: mouse

C/Species: Mus musculus (house mouse)

C/Date: 25-Feb-1994 #sequence revision 01-Sep-1995 #text_change 13-Aug-1999
C/Accession: S29170; S46209; S51173
R/Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.

Biochem. J. 289, 735-741, 1993
A/Title: Mouse synexin (annexin VII) polymorphisms and a phylogenetic comparison with ot

A/Reference number: S29170; MUID:93168121; PMID:7916616
A/Accession: S29170
A/Molecule type: mRNA

A/Residues: 1-463 <ZHA>
A/Cross-references: EMBL:L13129

R/Zhang-Keck, Z.Y.; Srivastava, M.; Kozak, C.A.; Caohuy, H.; Shitvan, A.; Burns, A.L.; F
Biochem. J. 301, 835-845, 1994

A/Title: Genomic organization and chromosomal localization of the mouse synexin gene.
A/Reference number: S46209; MUID:94330961; PMID:8053909
A/Accession: S46209

A/Molecule type: DNA
A/Residues: 1-463 <ZHF>

R/Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.
submitted to the EMBL Data Library, May 1993

A/Reference number: S51173
A/Accession: S51173
A/Molecule type: mRNA
A/Residues: 1-144,'S',146-303,'A',305-463 <ZHW>
A/Cross-references: EMBL:L13129; NID:9293293; PIDN:AAA37238.1; PID:9293294
C/Genetics:
A/Genes: MGI:Anx7
A/Cross-references: MGI:88031
A/Map position: 14
A/Intons: 19/3; 87/1; 121/1; 142/3; 177/1; 208/3; 246/3; 303/3; 360/3; 386/1; 423/3
C/Superfamily: annexin VII; annexin repeat homology
C/Keywords: calcium channel; ion channel
F:163-234/Domain: annexin repeat homology <AX1>
F:235-306/Domain: annexin repeat homology <AX2>
F:318-390/Domain: annexin repeat homology <AX3>
F:394-463/Domain: annexin repeat homology <AX4>

Query Match 48.8%; Score 774; DB 2; Length 463;
Best Local Similarity 47.5%; Pred. No. 1.2e-42;
Matches 151; Conservative 68; Mismatches 99; Indels 0; Gaps 0;

```
QY 1 MAQVLRGTVTDPPGPERADAEITLRKMGKLGTDSESLTLTSRNSAORQETSAAFKTL 60
DB 146 MTQGTGTILPASNFPAMDADAILRKMGKGFDEQAIYDVVNSNDROQIKKAFKTM 205
QY 61 FGRDLDDLKSELTEGFEKLIYALMKPSRLYAYELKHALKGAGTEKYLTIISARTPE 120
DB 206 YGKDLIKDKLSLGNMBELIALFMPPTYYDAMSLRKMGAGTERVLIILCTRITQ 265
QY 121 ELRAIKQVVEEBEGSSLEDDVVDGTSYYQRMVLVLLQANRPDAGIDEAQVEODAAQLF 180
DB 266 EIRDIYRCQVLEFGDLEKDIRSDTSGHFERLLVSCQGNRDNQINNMQAQEDQRLY 325
QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRETSGLLEQLLAV 240
DB 326 QAGEBGLGDESCFNMILATRSFPOLKATMEAYSRMARNDLSSVSREFSGIVESGLKTI 385
QY 241 VKSIRSIYAIYLAETLYYKMGAGTDHTLIRVMSRSEIDLINIKERKKNATSLYSMT 300
DB 386 LOCALNRPAFPAERLYYKMGAGTDSTLVRIVTRSEIDLVOIKOMFQOMYOKTLGTMTI 445
QY 301 KGDTSGDYKKAALLLCCGE 318
DB 446 ASDTSGDYRRLLLAIVGQ 463
```

RESULT 21

L1312

N:Alternate names: Hydra vulgaris

C/Species: Hydra vulgaris

C/Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999
C/Accession: A42660; B42660

R/Schlaepfer, D.D.; Fisher, D.A.; Brandt, M.E.; Bode, H.R.; Jones, J.M.; Haigler, H.T.
J. Biol. Chem. 267, 9529-9539, 1992

A/Title: Identification of a novel annexin in Hydra vulgaris. Characterization, cDNA cto
A/Reference number: A42660; MUID:92250599; PMID:1339458
A/Accession: A42660

A/Molecule type: mRNA
A/Residues: 1-316 <SCH>

A/Cross-references: GB:M83736; NID:9159255; PIDN:AAA29206.1; PID:9159256
A/Accession: B42660
A/Molecule type: protein

A/Residues: 2-9,'D',11-30;246-251,'E' <SC2>
C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

deretocod.

C/Superfamily: annexin I; annexin repeat homology

C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F:2-316/Product: annexin IV #status experimental <MAT>

F:16-87/Domain: annexin repeat homology <AX1>

F:27-43/Region: endonexin fold #status predicted

F:88-159/Domain: annexin repeat homology <AX2>

F:99-115/Region: endonexin fold #status predicted

F:171-243/Domain: annexin repeat homology <AX3>

RESULT 23
 S70644
 annexin VII - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999
 C/Accession: S70644
 R/Stavitskaya, M.; Zhang-Xeck, Z.-Y.; Caohuy, H.; McPhie, P.; Pollard, H.B.
 Biochem. J. 316, 729-735, 1996
 A/Title: Novel isoforms of annexin in Xenopus laevis: multiple tandem PEGM repeats distal
 A/Reference number: S70644; MUID:96265035; PMID:8670145
 A/Accession: S70644
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-512 <SRI>
 A/Cross-references: EMBL:U16365; NID:G790543; PIDD:AA81845.1; PID:G790544
 C/Superfamily: annexin VII; annexin repeat homology
 F/212-282/Domain: annexin repeat homology <AX1>
 F/283-355/Domain: annexin repeat homology <AX2>
 F/357-439/Domain: annexin repeat homology <AX3>
 F/443-512/Domain: annexin repeat homology <AX4>

Query Match 44.1%; Score 706; DB 2; Length 512;
 Best Local Similarity 47.3%; Pred. No. 3.2e-38; Mismatches 103; Indels 2; Gaps 2;
 Matches 146; Conservative 60; Mismatches 103; Indels 2; Gaps 2;
 QY 6 RGVTFPPGDERADAEETLRKAMKGLGTDESIITLTLSRSMQROEISAFAFTLFGPDL 65
 Db 200 QGITKAPNFDALSDAEKLRKAMKGFIDEKPI-DVANSNDQROKIOAFKAYAKDL 258
 QY 66 LDDLKSLTGKFEKLIYALMKPSRLYDAYELKHALKAGATNEKYLTETIIASRTPEELRAI 125
 Db 259 IKOLKSLSGNVEBELITALEPSTYYDAWSLYNMKAGQGERVLEILCTFTNSELRNI 318
 QY 126 KQYEEBVGSSLEDVDVGTSGYQRLV-VLQANDPAGIDEAIVEDDPAQLPAGE 184
 Db 319 VACYKQEPGEIEKIDRSDTSIGHERLLISIMAGIYDESQNVMOQAEODAPQLPAGE 378
 QY 185 LKMGTEBEKFTITFGPSVSHLRKVPDKYMTISGFQIEETIDETSQNLLEQLLAAYKSI 244
 Db 379 GKIGTBESSNVLVASHSPQLKAVAEAVARISRDLSVIGREFSGYIEDGKAVLQCA 438
 QY 245 RSLPAYLAETLYYAMKAGTDDHTLLRWVSRSEIDLFNIRKEFRKAFATSLVSMIKGDT 304
 Db 439 INRPLFRDLCSMGAGCAGDSTLRIITRSEIDLVOIKAYVQYKSLSAIISDT 498
 QY 305 SGDYKALLLLCG 317
 Db 499 SGAYKRMLLAISG 511

RESULT 24
 S41022
 hypothetical protein T07C4.9 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C/Accession: S41022
 R/Berks, M.
 submitted to the EMBL Data Library, January 1994
 A/Reference number: S41014
 A/Accession: S41022
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-676 <BER>
 A/Cross-references: EMBL:Z29443; NID:g1067051; PID:g443836
 C/Genetics: 69/3; 161/1; 208/3; 227/1; 357/1; 505/3
 A/Introns: 69/3; 161/1; 208/3; 227/1; 357/1; 505/3
 C/Superfamily: annexin repeat homology
 F/373-444/Domain: annexin repeat homology <AX1>
 F/445-516/Domain: annexin repeat homology <AX2>
 F/528-600/Domain: annexin repeat homology <AX3>
 F/604-675/Domain: annexin repeat homology <AX4>

Query Match 44.1%; Score 706; DB 2; Length 676;
 Best Local Similarity 46.5%; Pred. No. 4.5e-38;
 Matches 146; Conservative 63; Mismatches 103; Indels 2; Gaps 1;
 QY 4 VLRGVTFPP-GPERADAEETLRKAMKGLGTDESIITLTLSRSMQROEISAFAFTL 61
 Db 357 VMICTPSVFVQGNNSADAEVLKAMKAGCNNSKVISILCQRTNMQROEISAFVYMY 416
 QY 62 GRDLDDLKSELTKGFEKLIYALMKPSRLYDAYELKHALKAGATNEKYLTETIIASRTPEE 121
 Db 417 GKDLIKELKQELHGFEDFDLILALMDAPAIYDAQHLHAGMGLGKESVLEIMSKRNAQ 476
 QY 122 LRAIKQYEEBVGSSLEDVDVGTSGYQRLVVLQANDPAGIDEAIVEDDPAQLPAGE 181
 Db 477 IQQVRDAYKMLFKXDLERDLIGETSGHFKELVSLCAGGRDESSQDTGLANDAPRLLQ 536
 QY 182 AGELKMGTEDEKFTITFGTSVSHLRKVPDKYMTISGFQIEETIDETSQNLLEQLLAAY 241
 Db 537 AGEKRLGTDESTNALIASQNFQSLRVFEYQKASNHSIEKAIIEFESGIDRIDGLAVI 596
 QY 242 KSIRPAYLAETLYYAMKAGTDDHTLLRWVSRSEIDLFNIRKEFRKAFATSLVSMIK 301
 Db 597 AVIRNRPAYFAKLDHSMKGLGTRDNDLRLCVTRAEDMGDIRNMFQSLYRTSLNEMIK 656
 QY 302 GDTSGDYKALLLL 315
 Db 657 GDSCGAYKEGLIAL 670

RESULT 25
 LUBO36
 annexin II - bovine
 N/Alternate names: 36k protein; calcium-dependent phospholipid-actin-binding protein; ca
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 04-Dec-1986 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
 C/Accession: A03081; S02477
 R/Kristensen, T.; Saris, C.J.M.; Hunter, T.; Hicks, L.J.; Noonan, D.J.; Glenney Jr., J.R.
 Biochemistry 25, 4497-4503, 1986
 A/Title: Primary structure of bovine calpactin I heavy chain (p36), a major cellular sub
 A/Reference number: A03081; MUID:87026517; PMID:2945590
 A/Accession: A03081
 A/Molecule type: protein
 A/Residues: 1-339 <KRI>
 A/Cross-references: GB:M14056; NID:G162778; PIDD:AAA30421.1; PID:G162779
 A/Experimental source: Madin-Darby kidney cell line MDCK
 R/Martin, F.; Derancourt, J.; Capony, J.P.; Martin, A.; Cavadore, J.C.
 Biochem. J. 251, 777-785, 1988
 A/Title: A 36 kDa monomeric protein and its complex with a 10 kDa protein both isolated
 n-severing properties.
 A/Reference number: S02477; MUID:88326216; PMID:2970844
 A/Accession: S02477
 A/Molecule type: protein
 A/Residues: 27-61 <MAR>
 A/Experimental source: aorta
 A/Note: 44-Lys was also found
 R/Glenney Jr., J.R.; Boudreau, M.; Galyean, R.; Hunter, T.; Tack, B.
 J. Biol. Chem. 261, 10485-10488, 1986
 A/Title: Association of the S-100-related calpactin I light chain with the NH2-terminal
 A/Reference number: A38844; MUID:86278112; PMID:2942542
 A/Contents: annotation; amino-terminal acetylation
 C/Comment: Annexin undergo reversible, calcium-dependent binding to membrane phospholip
 destood.
 C/Comment: Calpactin I, a tetramer of two heavy chains and two light chains, is found in
 okeleton and be involved with exocytosis.
 C/Comment: Annexin II is the heavy chain component of calpactin I. The affinity of annex
 n I binds two moles of calcium ion per mole of annexin II. These ligands make annexin II
 C/Comment: Annexin II may act as a regulator of intracellular phospholipase activity.
 C/Superfamily: annexin I; annexin repeat homology
 C/Keywords: acetylated amino end; actin binding; calcium binding; duplication; endoneixin
 F/2-339/Product: annexin II #status experimental <MAT>
 F/2-12/Region: calpactin I light chain binding
 F/36-107/Domain: annexin I light chain homology <AX1>

F;47-63/Region: endonexin fold #status predicted
 F;108-179/Domain: annexin repeat homology <AX2>
 F;119-135/Region: endonexin fold #status predicted
 F;192-264/Domain: annexin repeat homology <AX3>
 F;204-320/Region: endonexin fold #status predicted
 F;268-339/Domain: annexin repeat homology <AX4>
 F;279-295/Region: endonexin fold #status predicted
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F;24/Binding site: phosphate (Tyr) (covalent) #status predicted
 F;26/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 44.0%; Score 704.5; DB 1; Length 339;
 Best Local Similarity 46.3%; Pred. No. 2,4e-38;
 Matches 146; Conservative 62; Mismatches 106; Indels 1; Gaps 1;

QY	7	GTUVDPPGDERADAEITLRKAMKGLGTEBESITLLTISRNSNAQOEISAPFETLFGRLD	66
DB	25	GSVKAYTNFDEARDLANIETAIKTGVDEVTIVNLTIRSNEDQDIAFAVQRRTKEEA	84
QY	67	DDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK	126
DB	85	SAIKSALSGHLETVILGLKTPAQYDASELKASKMKGAGTDEDSLIEIICRTNOELQETIN	144
QY	127	QYEEYEGSSLEDVVGDTSGYYQRMVLVLLQANRDPDAG-IDEAQVEQDAQALFOAGEL	185
DB	145	RYYKEMTKTDLEKDIVSDTSGDFRKLIVALKGRAEDGSVIDYELIDQDARDLYDAGVK	204
QY	186	KWGTEBEKFTTFGTRSVSHLRKVPDKMTISGFQIEETIDRETSNLEQLLAVVKSIR	245
DB	205	RKGTDPVKMISITWERSVCHLQVFERKYSYSPYDMLESIKKEVKGDLNVAFLNVQICQ	264
QY	246	SIPAYIAETLYAMKAGDDHILIRVMSRSEIDLFINRKEPRKNFATSLYSMIKQDS	305
DB	265	NKPLYPADRLYDSMKGKGRDQVILIRIMVSRSEVDMKIRSEPKKYGKSLYYIIQDPTK	324
QY	306	GDYKALLLLCGEED	320
DB	325	GDYQKALLLYCGGDD	339

Search completed: March 25, 2004, 08:06:52
 Job time : 22 secs

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